

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGACACG CTAGTTTGAA CCAAAAGCAC ATCGACCGG CAAACGAACG GAAGAGACA	60
ACCGTGAAGA TGCTGAATC GATCGGACCA GGTCTGACCG CCGCGCTGC ANTCGGCGCC	120
GGTCGGCGCC GTCTGACTTC GATCATGACT GGCGGCCCGG TGGTATACCA GATGGAGCGG	180
GTCTCTCTTC GCGCGCACT GCGCTTGAC CCGGCAFCG CCGCTGAGCT CCGGACGCG	240
GGCCAGTTGA CCGAGCTGCT CAAGAGCTC GCGGATGCA ACCTGTCTGT TCGCAAGCAG	300
GGCACTCTG TCGAGGGCGG CATCGGGGG ACCGAGCGCG GCATCGGCGA CCGCAAGCTG	360
AAGAGGCGG CCGAGAGCG GAGCTTGCG CTGTCTTCA GGTGACCAA CATCGAGCG	420
CGCGCGCGG GTTCGGGAC CCGGAGCTT TCGGTCTGG GTCTGAGCT CTCTCTCGCG	480
GTCAAGCAGA AATGACGCT CCGGATCAA GCGGACTGGA TCGGTCTACG CGCATGGCG	540
ATGAGCTTC TCGAGCGCG AGGGAACCT ATTGGCGCG CGGCTTACG CTCTCTTCA	600
GTCTAGGCG CCGCTGCTG AGCGCTCAT GTGAGACTY CCGCGCTGA GCAGGTCG	660
GTCTCCGCG GAGGCGAGCG ACTCGCGCT GCAGGCGCT CTCGAGATAG GTCTCTCTC	720
GGCAGCAGG AAGAGCGCG NCTCGCTCT TCTCGCTCT GATGA	766

(x2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

- (a) LENGTH: 752 base pairs
- (b) TYPE: nucleic acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCTATGCG ATGACATCA CAGTATGCT AGGTATAGA CGACTCTCT CTCTCTGCG	60
GACTTCTCA GAGAGCTGA CCGTCTTTC CAGCGGCTA CAGAGAGCG GGTCTCTGG	120
GTGAAAGCG TCCGCGCGG CTCGCTCTG CTGCTATCA AAGAGGCGG CAAGCGCGG	180
TCCCGGTTG TACTTGACCA AGGATATAG TCGCTCTTC GGCATCGGA CAGAGACATA	240

TTTCTGAGCG	AGGTGACCGT	GAGCCGTGCG	CATGCTGAAT	TCCGCTTGG	AAACACGAA	358
TTCAATGTGG	TGGATTTCGG	GAGTCTTAAC	GGACCTACG	TGAACCGGGA	GGLLCTGGAT	360
TGGCGGTGCG	TGGCGAAGCG	CGACGAGTC	CAGATCGACA	AGCTCGCGTT	GGTGTTCCTG	420
ACTGAGCCCA	AGCAAGGCGA	GGATGACGGG	AGTACGGGGG	GGCGGTGAGC	GCACCGUATA	480
GGCCCGCGGT	GGCGGGGATG	TGGATCGGGG	CGCTGCTCGG	ACGTGCTAGG	AGCGGATTTT	540
GGCGGATTC	GACGATCTCC	AGGATTCGAT	TCTTGAGAGG	GTTGAGCGTC	AGGATGAGCC	600
CGCGCGGGCG	CTCATTCGCG	GGTGTGGCGG	GGTTTCGCCC	CTTACGACAT	GGCGCGCGCG	660
TGGCAATTC	TTTCTTCGCT	GGCGGAGGAG	GGACGCTTAN	CTTGGCGGCT	GAGAGGCTTA	720
TGCGGGGGCG	TTGCTGAGAA	CGCTGCGCG	CT			752

(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCAAT	AGCATGCGA	TGATCTTT	AAATGCGGAG	CGCATGCGCG	CGCTCGAGCA	60
CGACCGGACA	CGGGCGGCGA	TGGATCTGCT	AGCTTGAGTC	TGGTCAGGCA	TGCTCGTCAG	120
CGACCGGATG	CGCATATTTT	GTGCTGCACT	CAGATATCGG	GCGAATCGCA	TCTGCGCGCT	180
GGCGCGGGCG	GTCTGCAAA	CTACTCGCGG	AGGAATTTCC	AGTGGCGCAT	CAGATCTTTC	240
ATGCTGCTCA	CGGCTGTGCT	TTTGTCTGCT	TGTTGCGGTC	TGGTCAGGCG	CGCGCGGAGG	300
AGTACTGCG	AGGATTTGAA	AGGCGGCGAT	AGCGCGGAGG	CTTGCAGAT	TCAATCTTCC	360
GACCGCGCT	ACACATGAA	CATCAGGCTC	CGCACTTACT	AGCGCGGACA	GAACTGCTTG	420
GAAATTTACA	TGGCGGCGAG	GCGCGGAGAG	TTCTTGAGCG	CGGCGGAGTC	GTCTACTGCA	480
CGCGGAGCGG	CTTACGAAAT	GATATCTACT	TGGCTGAGAT	AGCATCTCGG	GATACCGCGG	540
CTTGTAGCG	AGCGGCTGCT	CTTACGAGTC	TACCGAGAG	CGGCGGCGAG	GAGCTCAAGC	600
AGCATCTTCA	AGCGCTTCCA	TTGGGAGCGG	GCTATCTGCA	AGCGGAGTAC	CTATGAGAGC	660
CTTGGCGGCG	CTGACATGCA	TGCTGCGGCA	GTGCTCTTCC	CGATTTGTCG	AGGATGAGCT	720

GAGCAACSCA GACCGGACCA ACWGGTATCG ATAGCGGCCN AATGGGGCT TGGAACCCNG	780
TGAATTATC ACAAATTCGG AOTACNAAA NAA	813

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGTATUAAAC AGGCGGCGCT CGATAACTT CGAGCTGTCT CAGGCTGGGC AAGGATTCCG	60
CATTGCAATC GGGCAGGCGA TGCGGATCGC GGGGCAGATC CGATCGGTCG GGGGTCAC	120
CACGCTTCAT ATCGGGGCTA CGGCTTCCTT GGGCTTGGGT GTTGTGACAA ACAACGGCAA	180
CGCGGCACGA ATCGAAGCGG TGATGAGGAG CGCTCGGCGC GCAATCTCTG GCATCTCCAC	240
CGGGACATCG ATCGCGCGCG TCGACGGCGC TCGATCTAAC TCGGCACCGC CGATGGCGGA	300
CGCGCTTAAC GGGCATCATC CGGTGACCTT CATCTCGATG AACTGGGAAA CCAATCGGCG	360
CGGACCTCCT ACAGGGAAGC TGAAATTGGG CGAGGGAACC CGGGCTGAT TTGTCGCGG	420
ATACCACTCG CGGCGCGCC AATTGCA	447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCACCTAC GGTGCGGAG TATGTGCGCC ACCAAATGTC TGCGAGCGGC CCAACGGAAT	60
CGGTGATCC GACTGCGAG GTTGTGGAAC CGGCGCGCGC GGAATATATC GTTCATGCTT	120
AGCGCGCGCA CGGCGAGCGC CGGATATGCG CGACTGAGGA GCGGCGGAAT TTGCGCGGCG	180

CCGCCGACGG	NGAGCGCCGG	AATGGCGGGA	GTGAGGAGGT	GGCAATCAT	GCCGAGKGTG	248
ATCCAAATCA	CGTGMATTCG	GACTGNGGKH	CGATTGAGC	ATCGAGGTAG	TGAGCGCAAA	308
TGAATGATGG	AAACCGGGG	GNGACCTCCG	NIGTCTCTGT	CGTGATAGT	GCTGTGCTGG	368
KGTGNGGNT	ATCGAGATGT	TCTTCGCGA	AACGTGATG	CGAGGAACAG	GCTGTCGG	428
NRAGGCGNAN	GCHGTGCHN	CGGNNNTTC	TGCHGCHNAT	CANAGAGKAG	ATTGATGCA	488
NAAGKCGTG	GAGGAGGNN	AATGCHGGR	CGGAGAGAG	GGNAGGCGAG	NRGCHTNGT	548
NNNTNTTNC	AGNNNNNTG	NGGNGGNGH	NRNCAAGCH	NTNNNGNAA	NGGNTTGT	608
GAAT						668

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCAGATCG	KAGCGCTCA	CTAAGGGGA	CAGAGCTTG	AGTCCAGCG	CGTGCGCGG	68
CGCTCAGAA	CTAGTGGAT	TTTCKGKGTG	CAGCAATTC	GTCAGGAGT	TAGKACAGTC	128
TAGCGGTCT	GTACGCTGA	TGCAATGAG	GACGACATC	TGCTGATGA	CAGGAGGAA	188
CGGTCGGA	CGTCAAGT	CAGCGCGG	CAGTCCGTA	ACCGCTCTC	CGCGGCGTA	248
CGGATCGGT	TTTGGGGH	TTTGGYCGA	CGCGAGYCG	ACGAGACAT	CGAGCTGTC	308
ATCTCAAGG	GGGCGATCG	GATGTTCTG	CGCGGACTG	ACGTCAGGT	AGTGGCGCG	368
GCAGACCGG	CTGCGGACA	TCTCAGGCG	GTGCGGAGG	ATGACCAAG	CGGTGATCGG	428
CGGATGAC	CGGCGCGCG	TGAGCGCGG	GTGCGAGTG	GGCTGTACT	CGAGCTCTT	488
GATGCGGTC	GAGCAGCGG	GCTTCGCGA	CAGGCGGCT	CGGCTGCGG	TGCTGCGGAG	548
CTGCGGACT	AGGTGCTGT	TGCGGCAAAA	GCTGCGGAT	GGCTGCGG	CGTGCATGAG	608
CGTGCAGG	GACTGCTGT	CGTGCAGG	CGG			633

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(#1: SEQUENCE DESCRIPTION: SEQ ID NO:7)

CGAGAGGAGC GCGCGCGGAG AGCGCGCGCG AAGCGCGATC GAGCGAGGCC TCGCCAGAGT	60
CGCCACACAC CAGAGGAGAG TCGATTCATG AACTTGTGCA ACCATTTTGA GCGCGTGGCG	120
CGCGCGCGAG CGAGCGAGCG GGTGCGCGAG GTCTATGCGG AGCGCGCGCG GAGTTTGGGC	180
CGCGTGGCGG AGCGCGTCTC CATCTGTGCG CGGAGCGAGG GACTGCTGAC CGCGCGCTGG	240
CGAGGTTTGA CGAGAGCACT GCTGCTGCGC GAGTGGCGC GTGGCGCGCA GGAAGCGCTC	300
GAGCGCGCGG TCGCGCGCAG CTTGCGCTTC CTTGCTGCGC TCGAGCGACA CAGCAGCATG	360
CTGTACGCGG CAGCGCAAA CAGCAGCTGC CGCGCGATCT TGGCGCGCAC AGCAGCTGCG	420
GCGCGTGAAC GGAAGCGGCG GTATCTGCGC TGGCGCGCAG GAGCGCGAG ACCGCGCGGA	480
CGCGCGCGAC CGTTGCGGCG GAGTGTGCGC GCGCAATACC TGGCAGCGCG GGTGCAATTC	540
CAGTTCATCG CAGCGCTGCT CTTGCTGCGC CTGAGCGAAA CTTTCTGCGC GAGCGCGCGG	600
CGCGCGCAAC AGCTCATGCG CGCGCGCGCT GAACTGCTGT TCGTGGCGAA GGTGCGCGCG	660
GAGCATGCGG CGCGCTGCTC GAGCGCTGCG GTGAGCGCG GAGCGCTGCG GAGCATCTG	720
GAGTGGCGAA CAGCGTTCGA GCGCATGCGA GCGCGCTGCG CGCGCTGCG CAGCAGCTG	780
GAGCGCGCGC GCGCATGCG GCGCAGCTG GTCAGGTCGG TCGCGCGCTG CTTGCGCGCG	840
TGGCAGCGAG AGCAATGCGC GATGAGCGCT GCGTGGCGCA AGCAGCGCAC CGCGCGCTG	900
CGCGCGCGCG TCGAGCGCGC CAGCGCTGCT CCGCTGCTGA CGCGCGCTGCG CGCGCATGCG	960
GTGAGCGCGC AGCGCTGCG CGCGCGCGCA TCGCTGCTGA AGCAGCGTGC GCGCTGCTG	1020
GCGCGCTGCG CTTGCGCTG CTTGCGCGCG GCGCGCGCGA TCGCGCATGCG GATGCGCGCG	1080
GCGCGCGCGA GCGAGCTGCG GCGCGAGAG CGGAGCGAGT GAGTGTGCGC GCGCTGCTG	1140
TAGGCTGCGA TCGCTGCGCG GAGCGATGCG GCGCGCGCGA AGCGAGTGC CAGCAGAGCT	1200
GAGAGTGCAG CCGAGCTGCT TCGCGCGCGA GCGCTGCTG GCGCTGCTG TCGCGCGAGT	1260
GCGCGATGCG GCGCGCTGCG GCGCTGCGCG GAGGTCGCG CTAAGCGTGC GGTGAGCGAA	1320

GGACCGGACG GTCAACGGGG GTCAACCTTC GCGCCCAAGG AA 1362

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGAGCGACCG CGATATCCCG GGCACCTAG CGAAGACCT CCGCGACCA CTCGGGCGCG	60
GTATGCTCC CTTGAGGAC ATTCAAGACT GCGGAGGCG CCGGCTGGGG GAGGCGCGTC	120
TGATGACCT GCGCGCTGT TACATCATCT AXCAGGAGG GCGGCGCGAG CTCGCGACCG	180
CTAAGCGTT GTCGCGCTG CCGGAGGACT TAAAGCTGAG CTTGCTGGCG GTGACCGTAC	240
TGCGCGCGCG CTATCTCTCG CAGGAGGAG GCGGCGCGCG GCGGCGCGCG ACGGCGCGCG	300
TGATGACCG ATCGCGCGCG TGTCTCGCG GCGGCGCGCG GCGGCGCGCG CCGGCGCGCG	360
CGAGCGCGCG GCGGCGCGCG TGTCTCGCG TATTACGAA CTTGAGATTC CTGCGGATTC	420
CGCGCGCGCT GATGAGCTCT GGCACCGAG TGGGCTGCT CCGGCGCGCT TTCTCTCTCG	480
CGATTTAGCA TTCTCTGCA TCGATCTTC CGAGCTGCG ACAGCGCGCG GAGCTGAGCG	540
GCGGCGCGCG GCGGCGCGCG TATGCTTCA GGCACCTGCG ACGGCGCGCG GATCGGCTG	600
CGCGCGCGCG GCGGCGCGCG TGTCTCTTC ACGGCTGCT GATGAGCTG	660
CGCGCTGCT CTCTAGGCG GGTCTCGCG GTGCGGCTG TATGCTGCG CTGATGCTG	720
GCGCGCGCG TATCTGAT TTCTCTGCG GCGGCGCGCG ACGGCGCGCG GAGCTCGCG	780
ATTCAAGCT ATGCTGCTG GTGACCGAG CTTCTCTCG GCGGCGCGCG CCGGCGCGCG	840
TACGCGCGCT GGTGATCG CGAGCTGCG AGATCTCTCG GCGGCTGCG GCGGCGCGCG	900
TGTTGAGCT CATCTGCGA GCGGCGCGCG GCGGCGCGCG TCGGCGCGCG GGTCTCTCG	960
ACAGAGTCA TAGGCGCGA GCGGCGCGCG GCGGCGCGCG CATGAGCTG ACGGCGCGCG	1020
GCGGCGCGCT CCGCTCTCG CTTGAGCTG CATCTATCT GCGGCTGCG ACGGCGCGCG	1080
GATCTCTCG GCGGCTGCG GTGCTCTCG ACGGCTGCG GCGGCTGCG GGTCTCTCG	1140
TGCGGCTCTG TGATGCTCG ATGATCTCA GCGGCTGCG CTTGCGCGA CTGAGTGAAG	1200

CGGCGCGCGG CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTGCGCGGGA CTGCTTGCCG	1260
CACTCGGTAT TCCTTGGGAC AGTGAGGAGG CGSTGGGGTT AGCGACCGGG CTCATGGGTC	1320
GCATACACCA GCGCGCGGAC ACCGCATCGG GGAAGCTGGC CGAGAGCGGG CGGCGATTCC	1380
CGCGCTTCAC GCATAGCGGG TTGCGCGGCT CGGCGCGGAG GCGCAGCGCA GAGCTACCT	1440
CGTGGCTGCG GAGGCGGA	1458

(1) INFORMATION FOR SEQ ID NO:9:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCGTTATAT CGTCGTGAT CTGGACCGCG GTGGCGCGGT ACCTACGGAG ATCTACTGCG	60
GGCGCAGGAG CGTCGCGCTG GGCATCGCGG TCTTCGTTAT CGGGATCGCG CTGGCCATCG	120
TCATCGCGCT GTGTGACAGC AGCGCGGCTG CAAAACCGGT CAGCGCGCGC AAGCGCGGCT	180
CGCGCGAGAG CGTCCGCGG CTGCGCGGAC CGCAGCGACC CGAGCGCGCG GGCAGAGCG	240
AAGTTAAGCG GCGCGCGCGG CGGCGCGGAG GCGAAGCGC CGAGAGCGCG AGCGCCACCG	300
CGCGCGTCCA GCGCGCGCGG GTGCTCAGCG AAGCGCGGGA TTGCGCGGAT TCGAGCGCTG	360
CGGTCAAGAG TTGACCAAG CGCGCGCGAT ACTACTCGCG CGAGCGCGCG AACTTCACCA	420
TGGTGGTCA CACATCGCG CTGTTGTCTT TTAAGCGGA CGTTGCGGCG CGGTCTTGG	480
CGCGCGAGCT TTACTCGCTG GACACAGAGC GGTGTGAGTC CAGCGCGGAG TCGCGCGGCT	540
CGAGTGAAGC GTGTGCGAG ACTTTTCTCT CGGTGAGGCA GGTAAAGGAC CGGTGAGCT	600
GAGCGCGGAT CGGTTCGCG CGCGCGTGGC CATTCGCGG CGCGCGGATC GCGCGCGGCA	660
CGTACGATCT GGTGTGAGAG CTGGGAGATC TCGCGCTGCT GCGCGTGGCG TTGATCGTGA	720
ATCAGCGCGC GCGCGCGCGG GCGCGCGTAC CGGTCTCGGG TCGAGCGGAG CGCGCTCGCG	780
CGGAGTTCGC CGGCGAGGCG GGTATATTAT TGTGCGTGA TGTGCGATTG CGCGAGCTGT	840
GACAGCGGCT CGGTGCTGTC CG	862

(1) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCGACA CCGCAAGGC GTACATGTC TCCCTGGTTC TCGAGTGGC CAATCAGAA	60
GACACCCCGG GAGCGAAGAT GGTGCAAGTA GTGGCCGGTG GTGCTGCCG GAGCGCTGGA	120
GTGCGCAAGC GGTTCCTTGT CACCAAGGTC GATGAGTCCC CGATCAACAG GCGGACCGCG	180
TTGCTTGTC CCGTCGGTTC CAAGGCGCG GCGCGCAGCG TGGCGCTAAC CTTCAGGAT	240
CGCTCGCGCG GTAGCGGAG AGTCGAGTTC AGCTTCGGCA AGCGGAGACA GTGATGAAG	300
TGCGCGGCG GTCTTCAGT CTCTGATGTA CGCTGAGACC CATGGAACAG GATGCGGAT	360
TGCTGCTTC CCGGCACCTT GTCTGTCTC TTGACGATC GACGCGGAC GCGCATGAAG	420
AGCAACCGCG GCGGCTTGT ACCGAGTTC TCACCGAGTC CGGCTTCTTT GTGAGCGCG	480
TGCTGGGCT GTTGGCGGAC GAGTTCGAGA TCGGAATTC GCTGAGACA GCGGTGATG	540
GCGGGGTGGA CTTGCTGTG TCGCTGCGG GCGCGGAT GTGCTCTCG GAGTCAACC	600
CGGAGAGTTC CGGAGATTT CT	622

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGCGCGCG TAGGCTGTT GCGCGCGGAC AGCTTGGTGT TGACAGATG GCGCGTGGC	60
ACCAAGAGCT GGTGTGAGG GCGAGCGGGA AGCTTGGT GTTGCAGTC GCGCGGACG	120
AAGAGCTGC ACTCAGCGG CTGAGCGGGA CAGGAAATG CGATGAGCA GTTCTCTAT	180


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GGCTACGTGC GATCTGCGCC GGGCTACACG TTGGACTACA AGCCGACGG GTGCGGTGCT 245
GGGTGTAGCC AGTTCTGAA GAGCGAAGCC GATTTCGCG GCTGGGATGT GCGTTGGAAT 300
CCCTCGACGG GTCAAGCTGA CCGGTCGGTG GAGCGCTGC GTTCCCGCGC AFGGACGTC 360
CGACGGTGT TCGGCGCAT CCGGATCAC TACAATAICA AGGCGGTGAG CAGCGTGAAT 420
CTTGACGAG CCACTAGCG CAGGATTTT AGCGGACCA TCACCGTGT GAATGATCCA 480
CAGATCGAG CCTCTACTC CGGACCGAC CGGCGGCAA CAGCGATTAG GGTATGTTT 540
CGCAGCGACA AGTCCGTAC GTGCGACAC TTCCAGAAAT ACCTCGACGG TGATCGAAG 600
CGGCGGTGG GCAAGCGCT CAGCGAAGC TTCAGCGGG GCGTCGCGT CCGCGCGAG 660
GGGACAGAG GAGGTGCGC CCTACTGCG AGCAGCGCG GGTGATGAC GTAGACGAG 720
TGTCTTTT CCGTGGTAA GCAGTTGAA ATGCGCGAG TGTCTGCT CCGCGGTCT 780
GATCGGTCG CGATGACAC CGATGAGTC GTTAGACAA TCGCGCGCG CAGATGATG 840
GGACAGGCA AGGCGCTGT ATTGGACAG TGTGCTGTT AGGAGCGAG CAGCGCTGG 900
TCTTAGCGA TGTGTGTCG GACCTATGAG ATGCTCTGT GAAATACCG GATGTCGCG 960
ACCGTACTG CGGTAGCGC GTTATGCAA CGCGGATTC GTTCAGCGA AGAGGCTG 1020
GACCAATAG CTTGATTCG GTTCCGCAA TGTGTCGAG CAAGATTGG GCGCGCTG 1080
AATCTATTT CTGACCTAG TTAGGGAAT TCGAGGTGA GCGTCCCTT TCGGAGATA 1140
CGTCTGAT TTGGTCTTA TCGCTATTG CCGTCTCTG CGGAGCGAG GATGCGGAG 1200

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(2) INFORMATION FOR SEQ ID NO:12:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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GCAAGCAGT GAGGTCGTG CTGTTGAGC ACTCTGCAAT GCGAAGCGC AAGTGTACCA 60
AGACCGGTA CACCAAGAT GCGACGGCG TCGATCGTT GTTGACAGG ACCGCGATC 120
CGTTTGCA ACATCTGTC GCGCAGGCG ACCTGALCG GTTCAAGTC ACCGTCGCG 180

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GTTTCTCTCA AGCGTGGCC GCGACGCCC GCATCCACAC CAGCTTCAC CAGACGATCG	246
CCGCGACCGG CGCGCTCTC TCGACCGAAC CCGACCTGCA GACATCCCG ATCGCGACCG	300
ACCGGGCCCG GCGGATCGG GAGCGCTTCG TGGTCGGGA CGCTTACGC CAGTTGATGA	360
CGCGCGACTA CAUCAGATC GAGATCGGG TCATGGGCA CTGTCCGGG GACGAGGGCG	420
TCATCGAGCG GTTCAGACG GGGAGGACG TGTATTCCTT CGTCCCTCC CGGTCTTCG	480
GTCTGCCAT CAGCGAGTC ACCGGCGAT TCGGGGCGG GTCGAGGCG ATGCTCTAG	540
CGCTGGTTA CGGCTTACG GGTACGCGC TGTGAGGA GTTGAAATC TCGACCGAGG	600
AAGCCACGGA GCAGATGCG CGGTATTTG CGCGATTGCG CGGGTTCGU GACTGCTGC	660
GGCTGCTACT CGAGCGGGC GCGAAGGCG GCTACGCTC GAGGTTGTC GCGCTGCGC	720
CTCTCTTCC CGAGCTGAC AGCAGGACT GTCAATGCG GCGGGCGCG GATGCGGCG	780
CGCTGACCG CGCTATCGG GCGAGCGGG CGGACTCAT CAGGTGCGC ATGATCGAG	840
TGACGAGCG GTTAAAGAG GCACAGCTG GGTCCCGAT GGTGCTGAG CTCGACGAG	900
AGCTGCTGT GGAATGCGC GCGGTGAC GCGAGCGGT CAGCGCCCG GTGCGCGACA	960
AGATGGCGG CGCTTACCG CTCGAGCTC CGCTGAGGT GTCTGTCCG TACGCGCGCA	1020
GTGCGGAGC GCGCGCGCG TGAGTGGCG GGTGATGTC GCGCGGGA TTCGCGATT	1080
TTTCCGCGC GAGTTACCG TGAGGCAAT CGAGGCGAG TTTGTGAGC GTGACCGCT	1140
CGAGTACCT CTCG	1155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCGTC TGGTGTGAG AGGATTTCG CGTCCGCTC CGGACGAGG GTTCCCGGT	60
TGGGCTCTG GGTGGGATC GTCGAGGAG GTGCTGCTA AGCAGGCGG ATTGTTGGG	120
ATCGAGGACA CGGCTCAGG GCGCGAGCG CGTGGAGCT CGATTTCAT GCTGCTCCG	180

GGCGGTGGGA TGCGGATTCG GCGAGTTCCG GGTGGGACCG CTGGGCGTGG GAGCAGGGAC	240
ATCGAGAACT CTCGGGATTC GCGGAAAGTT ATCTCAGTGG AATCTCACTC CAGCCGCGCA	300
ACCTAGTTGT GCAGTTACCG TCGAAGGCGA CAGCAATGCC AGTCGACCTA TCGCCAGATT	360
GGCCCAAGTA GTGGGCTTAG TACGCGAAGA GCAACCTTAG GACATGACGA ATCAACCCAG	420
GTATTGCGCA CGGCGGACAG AGCGCGGAGC CCGAGTTTAT GGTAGGAGGC AGGACCAAGC	480
GTACAGCGAG CAGTTTCACT GCGCTTAGCC AGCGTCCCGC CCGTGGCGGC CAAGCCAGTA	540
CGCTCAACCC TACGAGCGGT TGGGTGATAC CTGGCGCGGT GTGATACCTG GGTGATTCC	600
GACGATGAGC CCGCTGCTG GAGTGGTTGG CCGAGCGCTT CTGCGAGGCA TGTTCGCTAT	660
CGCGGGGCTG AGGATAGCGG TGGTGTGGGC CGGCATCGAG GCGCGGCGCG CATCTCTGGT	720
CGGGTTCAAC GGGGCAAGCG CCGGCTCCAG GGGAGGCGCA GTGGCTGCGA GCGCGGCGCC	780
AGCGATCCCG CGAGCAACCA TCGCGCGGCG GTCGGTGAAA CAGGTGCGCG GCGAGTTGGT	840
GCGCAGTCTC GTCAATTTGG AAGCGGATCT GCGCGCGCGC TCGAGAGGAG GCTCGCGCAT	900
CATTCTGCTC GCGGAGGCGT TGATCTTCAG CAACAACCGC GTGATCGGCG CCGCGCGCAA	960
GCTTCGCTG GCGAGTCCCG CCGCGAAGAG GAGGCTAACC TTCTCTGAGG GCGCGAGCGC	1020
ACGTTTCAGC GTGGTGGGCG CTGACCGGAC CAGTGATATC GCGGTGCTCC GTTTTCAGGG	1080
CGTCTCGGCG CTGACCGGAG TCGCTCTGGG TTCTCTCTCG GAGCTGAGAG TCGGTGAGCC	1140
GCTGCTGGCG ATCGGCTGCG CGTGGGTTT GAGGCGGACG GTGAGCAAGG GAGTCTGAG	1200
GCTCTGAGC GGTGAGTTGT CGAGGACCGG CGAGGCTGCG AGGAGAGACA CCGTCTGAG	1260
CGCGATTGAG AGGAGCGCG CAGTCAACCC CGTAACTCC GCGGGTGGCG TCGTCAACAT	1320
GAGCGCTGAA CTCTCTGGAG TCAACTCGGC CATTCGCAAG GTGGGCGGCG ACTCAGCGGA	1380
TGCGAGAGAC GGTGAGTTGT GTCTCGTTT TCGATTGCA GTGAGGAGCG CCGAGCGCAT	1440
GCGGAGAGAG TTGATGAGCA CCGGCAAGCC GTGAGTGGC TCGGTGGGTC TCGAGTGGAC	1500
CATGACAAA GACACCGCG GCGGCAAGAT GGTGAGTTA GTGCGCGGCG GTGCTGCGCG	1560
GAGGCTGGA GTGCGGAGCG GGTGCTTTGT CAGGAGTTT GAGGAGGCGC CGATCGACAG	1620
CGCGAGCGCG TTCTTGGCG GGTGCGGTC CAGGAGGCGC GCGGCGAGCG TCGGCTTAAC	1680
GTTCAGGAT GGTGCGGCG GTAGCGGAC ACTCGAAGT AGCTGCGCA AGGCGGAGCA	1740
GTGATGAGCG TCGGCGGCA GTGTTCAAG C	1771

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGCG	CTGGGCKXCG	CTCTAAACT	ATTGATCC	CGGGCTGCA	GGAATTCGGC	60
AGGAGATCC	GACGTCCAG	ATTGTGAC	CGGGCGGCG	GGAAGTATCG	GTGGATGGGT	120
ACCGCGGGA	CGGCGGCG	CGGAATCGG	CGAATGAGGA	GGCGGGAAT	TTGGCGGGCG	180
CGGGGAGCG	CGAGCGGCK	ATCTCGCG	GTGAGAGCG	GCGGAGTAT	GGCCAGGGTG	240
ATCCAAATCA	CTTGATTCG	GGTGGGCG	CGATTGCGA	ATCGAGGTAG	TGACCCGARA	300
TGAATCATCG	AAAGCGGCG	GTGAGGTGG	CTGTCTGCT	GGTGGTGGT	GGCTGGCTCG	360
GGTGTGGCT	ATCGAGTAT	TGTTGGCG	AGCTGATCG	CGAGGAGCG	GGTGTGGCG	420
TGAGGCGAG	GGGTGGCG	CGGGGCGCG	TGGTGGAG	CGGCGAGCG	CTTGTGGCG	480
CAAGGGGCT	GACGAGGCG	CAGTGGCG	TGGGAGGCG	CGGAGGCG	GAGGCTGGCG	540
TGGGTATTC	CAGTGGCG	GTGAGGCG	CGGCGAGCG	GGTGGGCG	AGGCGGAT	600
GGAGGAGCG	GGTGGGCG	TTGGGAGCG	AGGCGAGCG	ATCTGGGCG		660
AGTGTGGCG	CGAGGAGCG	ATCTGGGCG	CGATTGCG	ATCTGGGCG		720
TGGTGGCG	GGTGGGCG	AGGCGGCG	TGGTGGGCG	CAGGAGGCG	CAAGGCGAG	780
GTAGGAGCG	GGTGGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	840
CTGTGGCG	GGTGGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	900
AGGAGGCG	GGTGGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	960
TGAGGAGCG	GGTGGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	1020
GTGAGGCG	GGTGGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	CGGAGGCG	1058

(12) INFORMATION FOR SEQ ID NO:15:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA GGAGGGTGA TGGACATCT CGGACACAGC CCCACATCT GGGACAGGC	60
GGGGGGGAG DGGGTCCAGC GGGGGGAGA TAGGGTGGT GACATCCGC TGGGTGGGT	120
CATTGAGAG GACATGGGC TGGACGGGC CGGCAAGATC ACGTACCGCA TCAAGCTCGA	180
AGTGTCTTC AAGATGAGC CGGCGAAGC CGCTAGCAC GGGCGGGCA GCAGACCGA	240
AAATGGCAG GTTGGGGTT CATTGTTGC ATTTTGTGC TGTGGCGCA GGGCTACCG	300
GGGGGGGCA GGTGGGGTC GTGGGTATC CAGGGTGA TGGGATTC GGGAGCGAG	360
CCGAGTGA TGTGTGGT CGATCGAGC TGGGGGTC GCGGGGGG TGATCGAGA	420
CGGTGGCGC GGGGTGATC CGGAGTTC CGAGGAGAC GTGGTGGAG GCGGTAGCA	480
AGGGTGGCA GGGGGGGTC GTGGGGCT GTGGTGGC CCTCAGTTC GCGAGAGAG	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 913 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGGGAG GGGGGTGGC TTGGGGGAT TGGGGGGTC GCGATCAGC TGGGATGGC	60
GACCATCAG GGTTTTCCG GGGGAGGGC GGGTGGGG GGGGGGGCG ATGACAGGG	120
TGAGCTGCG CGGGGGGCG CGGCATTGG ATACAGGAG CGGGGGGGC CAGCTTACC	180
GGGGTGGCA GCGGGGGCG GGTGGGGTT TGGGGGGC GAGGGGGAAT GAGGGGGCG	240
CAGGGGGCG GGGGAGCG TTGGGGTT TGGGGGGC GGGGGGGC CGGCAATTG	300
CGGAGTGGC GGGGAGCG GGGGAGCG GGGGGGGT TGGGGGGC GGGGGGGC	360
GGGGGGGAG CGGCAATTG GGGGGTGG GTTGGGGC CGGGGGTTC GGGGGGGCG	420

GTTCCTCCG	AAATATCGG	GGGACCCG	AGACCCGCG	GGCCACCAT	TGCGCCGCG	480
CACCGAACA	ACAATCCAA	GGTGGCGCG	GGCGCGCGT	TTGGCGCAT	CACCGCCAT	540
TCACCGCG	CACCGCGGT	AATGTTATG	AGCGCGTAC	CGCCAGCGG	CGCCCATAT	600
CGCGCGCGG	GAGCGGTG	CGCGCGCG	CGCGCGCG	CAAAAGCGG	GGGTTCCAC	660
CGCGCGCGG	GAACCGCG	GTTCGCGG	TCCCGCGGT	CGCGCGCGG	CGCGCGCAT	720
TGCGCGGT	GAACCGGT	CGCGCGGT	CGCGCGGT	CGCGCGGT	CGCGCGGT	780
CGCGCGGT	GTTCGCGT	AGCGCGGT	CGCGCGGT	GTTCGCGT	TTCCCGCAT	840
TGCGCGGT	CGCGCGGT	CGCGCGGT	CGCGCGGT	CGCGCGGT	CGCGCGGT	900
CGCGCGGT	CGG					913

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACCTG	GTGTAGAA	ATCTGGCG	CGGACCGT	AGGCTGGA	CAATTCGA	60
TGCTACCG	GACACGAG	GTACCGGT	GACCAATG	CGGCGCGT	CATCAGCG	120
GTCTCTGT	CTGAGCTG	TGCTGCGT	CGGCTGCG	CTGCGCGG	CGCGCGCG	180
CGCGCGCG	CGCGCGGT	CGCGCGCG	GTTCGCGG	TTCGCGCG	TGCGCTGA	240
CGCGCGCG	ATGCTGCG	AGCTGCGG	ACAGTGGT	AACATGAA	CGAATGGA	300
CTACACAC	CGCGCGCG	CGCGCGCG	CATCTGAT	CACTGCAAC	GTCTCTGT	360
GCGAACAAC	CAGTGTAT	CGCGCGCG	CGGCTCAAT	CGCTCAAC	TGCGTGGG	420
CGAAGCTAC	CGGCTGAT	TGCTGCGT	TGCGCGCG	CAGATGTG	CGGCTGGA	480
GTCTCTGT	CGGCTGCG	TGCGTGGG	CGCGTGGT	CGGCTGCG	CGGCTGGA	540
CGCGCTGCG	CGATGCGG	AGCGCGCG	CGGCGCGG	CGGCGCGG	CGGCTGCG	600
CAGGCTGCG	CGGCTGCG	AGCGCTGCG	CGGCTGCG	CGGCTGCG	CGGCTGCG	660

GACATTGAAC	GGGTTGATCC	AGTTGGATGC	GGCAATCCAG	CCCGATGATT	CGGGCGGGCC	720
CGTGGTCAAC	GGCTAGGBC	AGTGGTCCG	TATGAGACGC	GGCCGCTCG	ATNACTTCCA	780
GCTGTCCAC	GGTGGGAGG	GATTGGCCAT	TCCGATCGGB	CAGGCGATGG	CGATCGCGGG	840
CCAAATCCGA	TGGGTGCGG	GGTCACTCC	GGTTCATATC	GGGCTTACCG	CCTTCTCTCG	900
CTTGGTGTGT	GTCCACACGA	AGGCAACGG	CGACAGAGTC	CAACGGCTCG	TGCGAAGGCG	960
TCTGGGCGCA	AGTGTGGGCA	TCTCCAGCGG	GGAGGTGATC	AGGCGGTCG	ACGGGCTCTC	1020
GATCAACTCG	GGCAGCGCA	TGGCGGAGCG	GTTTAACTCG	CATCATCTCG	GTGACTCAT	1080
CTCGGTGAC	TGGCAGACCA	AGTGGGCGG	CGGGCTTACA	GGGACCTGTA	CATGGGCGCA	1140
GGGACCCCG	GGTGTGTTG	TGGGGATAC	CACCGCGCG	CCGGCCATT	GGATTGGGCG	1200
CAGCGCTGAT	TGGCGGTGA	GGCGCGGAT	TGGGTCTGCT	GTGGGCTTGG	CATTGTGGAA	1260
GCATGACCG	AGCGGACCA	CAGGTGAG	CGGCTCTCG	TGGAGGCGCA	TTAGCTCGAA	1320
GGCGGTCTGG	TGGAGCTCG	GGATGCAAG	GACTTGGCA	GGCGGCGCG	CGTGGGCGCG	1380
GATCGGACTT	GGTTTACGA	CGCGCTTTC	TAGGAGGTGC	TGGTNGGCG	GTTCTTGGAC	1440
GGCAGCGGG	AGGTTTGGG	GGATCTGCT	GGATCATTC	ATCGGCTGTA	GTAGTGGCAG	1500
TGGCTTGGCA	TGGAGTGGT	CTGTTGGCG	CTTCTTACG	ACTACCGCT	GGCGAGCGCG	1560
GGTTAGACA	TTCGGACTT	GTACAGGTG	CTGGCGGAT	TGGGAGCGT	CGAGATTTTC	1620
GTGGCGCTGG	TGGAGCTCG	TGACCGCGA	GGTATCGCA	TGATGCGCA	CGTCTGTGTC	1680
AATCGAGCT	GGAGTGGCA	CGGTTGGTT	CAGGAGTTC	GGCGGAGCG	AGAGGAGCG	1740
TAGGCTGACT	ATTAGGTTG	GAGGAGGCG	AGCGAGGCT	AGCGGAGCG	CGGATGATC	1800
TTCTGCGACA	CGAGAGGTC	GAGTGGTTC	TTGATCTTC	TGGGCGGCA	GTTTCTACTC	1860
GGAGGATTC	TT					1872

(2) INFORMATION FOR SEQ ID NO:18:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1887 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGCGGAA AGCTGATGCG GAGGAACAGG GTGTTCGGGT GAGCGCGACG GCGTCCGACC	60
CGCGCGTCTT CGCGGAGATG AGGCACTGCG TTGATCGGRC AAAAAGGTTG ACCACGCTGC	120
ACGTAGCGGT GCGAACACCG GGGAAAGTCS ACAGCTTCTT GGGTATTACC AGTCCCGATG	180
TGGACCTTCC GCGCAATCG CTCCGCGCA AGGGCGTATG CAGCTACAC GAGGAGCAGG	240
CTGTGCGGTT TCGGGTACAA GCGGACACCA TCTCGGTGGA ACTGTTCGAC GAGTGGAGCA	300
ATCTCGGCTC GATTTCGAA CTGTCAACTT CACCGGTGCT CGATCCCTGC GCTGGGGTGA	360
CGCAGCTGCT GTCGGHTGTC AGCAACCTTC AGCGGAAAG TACCGAAGTG ATAGACGGA	420
TTTCGACGAC TAAATGACCG GAGACGATCG CGCGGAGTTC TGTCAAGATG CTTCATCTTG	480
CGCGCAGGAG TCGAAGGCGG GCGACCGTCT GGATTGCGCA GCGCGGCTCG CACCACTCG	540
TCCGAGCGAG CATCGACTTC GGAACCGGCT CGATTGAGCT CAGCGAGTTC AAATCGAAG	600
AAGCTGTGAG CGTCGAGTAC GCGGAAGTTC GGTGAGGCTG TTGCTGAAA GCGGCTTGTG	660
AAGCGTGTCA AGCGGACCGG AAATCTGACG CGCTGAGGCG ATCTGAAAA TGACCGCCCTA	720
GACCGCGGGG TGTGTGTTA TTCTTCGCTG GTTCGCGCTG GTGGAGTCCG GCGAGGTCG	780
CGGTATTGTA GCGGCTAGCT CTCGCTTTCG AGCGGAGCGA CTTCAGCATG GTGGACGAGG	840
CGTCTGCTCA TCGCGGAGCG AACGCGCTCG TCGCGCGCGA AAACCTGCGC CCGCGCGCGG	900
AAGGCTTAT TCGAGCTGAC GATCAAGCTG GCGGCTCAT ACCGCGAGGA CAGGAGCTCG	960
AAAGAGAGCT TCGCGGCGTC GCGCTGAAC GGAATGTAA CCACTTCCTC AAGCACCAGE	1020
AGCGGATAGC GCGCAACCGG GGTGAGTTCG CGGTAGATGC GCGCGGCGTG GTGAGCGCTCG	1080
GCGACCGCTG CTACCTATTC GCGCGCGGTC GCGAACGCGA CGGATGAGCT GCGCTGACAC	1140
GCGGCTATCG CGAGGCTGAC CGCAGATGTA GTCTTCGCGG TCGCAGGCGG GCGCGAAAAA	1200
CACGAGCTTA TCGCGGCGCG TGTATGAATC CAGGCTGCGC AGATGTGCGA TGGTGTGCGG	1260
TTTGAGGCGA CGAGCATGCT CAAAGTGGAA GTCTTCAAC GACTTCGCGA CCGGGAAGCG	1320
GCGCGGCGCG ATCGCGCGCT CAGGACGATG GAGGTCGCGG GCTGACACTT CCGCGTGCAG	1380
GCGCGCGCGC AGGTATTCTT CTGCGCTGCA GTTCTCGGCG GCGCGCGGAT CCGCGAGCGG	1440
CGCACTGAC TCAACCGGCG TCGCAKTTT CAATGCTCTT GT	1482

(2) INFORMATION FOR SEQ ID NO119:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCG	CGACCCGXX	ATAGCTTCTH	GGGAGGAGGC	GACCAATATG	CTGAGGGGT	60
CGTGTCTGGG	GCATCCGCG	GGGCACTCAC	CTTACCGGT	GAGGGCTTGC	AACACGCCAA	120
CGGTCACTCG	TTGTCTCTGG	AGGCAACGAA	CCGCGGCTG	CTTCACTTAC	ACCGGCGCTT	180
CGGCTACGAA	ATGGCTTACA	TCGGGGAAG	CGGCTGGCG	AGGATGTGCG	GGGAGAACCC	240
GGAGAACATC	TTCTTCTTCA	TCACCGTCTA	CAACGAGCCG	TACGTGAGCG	CGCGGAGGCC	300
CGGAGACTTC	GATCCCGAGG	CGGTCTCTGG	GGGTATCTAC	CGGTATCTAG	CGGCAACCGA	360
GCACCGCAAC	AACAGGNGC	AGATCTTGGC	CTCGGGGATA	GGGATGCCCG	GGGGGTGCG	420
GACGACGACG	ATGCTGGCG	CCGAGTGGGA	TGTCGGCGCG	GAGTCTGCTT	CGGTACCGAG	480
TTGGGCGGAG	CTAAGCGCG	AGGGGTGGT	CATCGAGACC	GAGAGGCTCG	CGGACCGCGA	540
TCGGCGGAGG	GGCTGCGCTT	AGTGGAGGAG	AGGCTGGGAG	AATGCTCGGG	CGCGGTGAT	600
CGGGGTGTGG	GACTGGATCG	CGCGGCTCCG	CGAGCGAGTC	CGACCGTGGG	TGCGGGGCAAC	660
ATACCTCAGC	TTGGGCAAGG	AGGGCTTGGG	TTTTTCGAG	AGTGGGAGCG	CGGTCTCTCG	720
TTACTTTGAC	ACCGAGCGCG	AATCGAGGT	TGGTGGGGT	TTTGGAGGGG	GTTCGCGCGG	780
TGAGGGGCTG	AATATCGAGC	CATTGGGTGC	CGGTCTGAGG	CGCGCGCGCG	AGTTACCGCG	840
ATTCAAGCAA	GCTGGGGGT	TGCGCGGAG	TAAGTT			876

(x) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGG	GGTCAAGGAA	TTGGGCAAGG	GAGACAAAT	TTCACCGGTT	AATGAGGGA	60
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CAGATTGATK ACGAATTGAC AGCGGCACAA CAATATGTG CGATCGCGGT TTATTGAGC	120
ADCGAGACCC TCGCGCGGT GCGAAGCAT TTTTACAGC AGCGGTGCA GGAAGGAAC	180
CATGGAATGA TCTCGTGA ACACTGCTC GACCGCGACC TTCGTGTGA AATTCGCGC	240
GTAGACCGG TCGAAGACC GTTACAGA CCGCGGAGG CACTGGCGCT GCGCTCGAT	300
GAGGAGCGC CAGTACGCA CAGGTCGCT CGGTGAGAG CGTGGCGCG CAGGAGGCG	360
GATTTCCTCG GCGAGCATTT CATGCAATGA TTCTTGCGG AACAGATGA AGAGTGGCG	420
TTGATGCAA CCGTGTGCG GTTTCGGAT CGGCGCGCG CCAACTGTI CAGCTAGAG	480
AACCTCGTC CAGGTGAAGT GGAATGCGC CGCGCGGAT CAGCGCGCG GCACCTGCG	540
GGGCGCGCG TCTAGATCG TGGCGGGAT CAGCGAGTG TCGCTTGGC CGCGCGCTCT	600
TCCAGCGAG CTTGCTGCG GCGCGGTG TCACTAGCA TCGAGCGAC CCGAGCTCG	660
CGGGAAGAT CAGTGTGCT GACTGCTG AGCTTCAGG AGTACCGCG CGCGCGCTCA	720
GCTCGCGAG GGTCAAGAG TTGCGGAT TCTTTAGC CAGCGAGTG GGTTCGAG	780
GCGATTGCG CAGCGCGCT GCGCGCTG CTGCTCAGT ATCGAGGCT CTTCGCGAG	840
AACAGCTCG CAGGAGGCG TCGAGCGCG CGGATCGCA GCGCGGCG GCGAAGCGA	900
CATGACACC GCGAGGATC GATTCGCG GCGCGCTCG GGAATCGCA AGCGTGTAG	960
GAGCGCAGC AGTTTGTTC CAGCGGCG AGCTTTTC GGTATCGAG GCGGTTAG	1020
T	1021

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGGCGAG ACGGAGGAA CACAGCATG AAGATGGTA AATCGATCG CCGAGCTCT	60
ACCGCGGCG CTGGAATCG CGCGCTGCG GCGGTGTGA CTTCATCAT GCTGCGCG	120
CGGTGCTAT ACGAGTGA GCGGTGCT TCGCGCGC CACTGCGCT GCGCGGGA	180

TCGGGCGGCG ANGTCCCGAC GCGGCGCCAG TGACCCAGNC TGCTCAACAG NCTGSMCGAT	240
CCACACGTCG CPTTGAGAA CAGGCGACAT CTGGTCGAGG GNGGATCGG NGGNANGAG	300
GGNGGATC GCGGACACA A	321

(2) INFORMATION FOR SEQ ID NO:22:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT TCGGTGGC GAGGGTTTT GGGGGCGGT GGTAACTGG CTGGCCAGC	60
CGATCGAGCG GCGGAGAGC GTCACTCTCT ATACTCGGC GCGGTGGAG CTCCAGGCGC	120
CGTCGGTGGT GACCTCCGAC GCGGTGAGG AGCGATGGA GACCGGATC GAGGCGATTG	180
AGCGATGAC CGCGATCGC CGCGGCGAC GCGAGTCAT CATCGGGAC CGCAAGACCG	240
GGAAAGACG CGGTCTGTGT CGGACCGAT CCTCAAGCA GCGGAGAGAA CTGGAGTCC	300
GGTGGATCC AAGAACGAG TGGGCTTCT TATACCTTG CCATCGGCA AGAGGGGAA	360
CTTACCATG CG	373

(2) INFORMATION FOR SEQ ID NO:23:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACCGCT CATCGATTC CTGGGAGGG CAGTCCGCT GCGGTGGTG GATCAGCAGC	60
TGCTACCGG GATGCGGAC GCGTGTCTAT TTGCTCAGC AGCGGCTGG CGGTGCTGT	120
TCTTACCGG CTGTTACGG TTGCGGATC TACCGAGAT CAGGCGGAG GATCGGTGC	180
TGATGATCC CGTACGTC GGTGTGGG GCGGCTGT GCGCTGCT GCGGAGTGG	240

GGCTGGAGGT TTCTGTACG GCCAGCGGTG GNAAGTGGGA CAGCGTGGCT GCGATGNGST	300
TTGACGACGA NCGATATGCG NGATTCCGCG ACATNGGAGG TTGCGANGGA GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(1) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCTGCG TTGATTCTCT TCGACCAGCG GGTGGCGATA ATCGCGGAG TGATCAAGCC	60
GGGTTCTGGG GGGGTCATGG GTCACGCGCA GTAATCAGCA AGTTCTCTGG TATAATGAC	120
CTAGCGTGGG GTTGGTTGGG AGATCGTTT CCGACCTCA TCGCATGTAC CGTTTGGGT	180
GAGGCACTCT GATGCTGGCG GCGTGCATCC TGGTCAAGGG TGTGGCGGAT CTGGGGCTCG	240
GCGGCGATCT CCGAGCGCAA ACCGCGCGCG TCGCTGACTA CTACTGGTGC CCGGGGACGC	300
CTTTGACCC CGCATGCGCG CCGACCTGCG ATCTCTACAG CTGCGATGAC GACTTCCACC	360
CGGACAGCGA CGGCTCGAC CACAGCGCGG ACTACCGCGG ACCGATCGCT GAGGTCGCG	420
TGCTTGACGA TCGGCTGCTT GCGCGCGCGG CTCTGCTGCG CGGTGCGGCG GGTATGCGCT	480
CGTTGACCGG CGCGCATCGG CGATTCGCG TATAAGCCCG GCGGTGCGCG CCGCAAGCTA	540
CGACCCCGCG CGGGCGAGAT TTAGCTCTCG GTGCGGATCG ATCGCGCGGT CGATTCGACG	600
AAATATGCGG AGGTTTTCGG CAGCGGCTTG GAGGAGGCTT GAAGGAGACT TGTCATGAGC	660
CGCGACGCGG CCGTCAAGAT CGAGATCGAC AAGGTTGTTA CCGGCAATAG GGTTCGCGCG	720
ATCGTG	726

(2) INFORMATION FOR SEQ ID NO:25:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACG	ACGAAGCTCG	GGCCGACGAC	CGCCTATGCG	TTGATGCAGG	CGACCGGAT	60
GGTGGCGGAC	CATATCTGAG	CATGCTGGCT	GGCCACTGAG	CGACCTTTG	ACGACCGGG	120
CTGCCCGATG	GCGGCGGCT	GAACTCATTG	CGCCGGGCT	TGTCACCTG	ATGAACCGA	180
ATAGGACAA	ATAGGCGCT	GATTTGGCAG	TTGATGCTG	GGTATGCTG	GAAATCAAT	240
GGCGGGCGAT	GTCGGGCGC	GACGAGGCTC	GCGGAGGCGC	GCGAGGCTGA	ATCTGGAAGG	300
AGCGCTCAAT	GGCGGCGATG	AAGCGCTGGA	CGGCGAGCG	TGCTTGGGA	GCAACTAGG	360
AGCGGCGCG	CATTGCGATG	CGAGTACCA	TTGAGGGTGG	CGGTGCGCTG	GTGCTGAGC	420
TGACACCGA	CGAGCGCGC	GCAGTGGGCG	ACGAACTCA	ACGCTTACT	ACCTAGAGC	480
AAGCGACCG	CGAATGCTG	CGCTAGCGG	CGACGCTCC	CGTAGATGCG	CAGTGTCTG	540
TGCGCGTGT	ATGCGGAGG	GAACTCTTGG	ATACAGCGCT			580

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGCG	CGCGGGGTT	TGCGGGGCG	GGGCGGCTG	GGGCAACG	CGGGCGGGG	60
GGTACCGCG	GCTTCTTGG	TGTGGGCGG	CGCGTGGG	CGGAGGCA	CGCATCGCG	120
GGTTCACG	GTACGCGCG	CAGCACCGG	GGTGGATCG			160

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA CGATGGTGGT GTAGGCCAAC GTTCTCGACA CGTCGAGGC GTTCAGGATC	60
CAGCCCGACAC CCGACGGGCT GACCATCGGC GATGCGGGCC GGTTCGCGGA GCGGGCTGCC	120
AAGGCGATGG GAATCGACAA GCTCGCGGTA ATTCATACCG GAATGGACCC GGTGCTGCC	180
GACCGGACAC AGTGGAGAGA CGGCAACAC ACCTTGGGCT TCGCGCGCG TGTGCTGTC	240
GCTACGAGC GCAACGTACA GACTAAGCCC CG	272

(2) INFORMATION FOR SEQ ID NO:29:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x2) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCACCGGGTG GTTCTCGGAC TATCTGCGCA CGGTGACGCA GCGGAGCTG CCGGAGTGA	60
AGCGGATCGA CGACACGGAT CGCTTGGGCC GGTTCATCGG CTACCTGGCC GGTATACCG	120
CGCAGGAGCT GAACGTGCC AAGCGGGCC GGTTCATCGG GGTTCGACCG GCGACGATCC	180
GTTCGATCT GCGCTGGTTC GAGAGGGTCT ATCTGGTACA TCGCTCGCC GGTCTGTCGC	240
GGATCTGAC CGCGAAGATC AAGAAGCGT CAAGATCCG GGTCTCTGAC AGTGGCTTC	300
CGGCTTGGT GCGGCGC	317

(2) INFORMATION FOR SEQ ID NO:29:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATGTTGGAG CTCTCGAIGA ACAGCGTTGC CGGCGCGCG GCGGCGAGCA GTTCGGTGA	60
-----------------------------------------------------------------	----

GCAGGCGCGG ACCAGCTGGC CGGTGGGAG CATGGTGAATG ACCAGCTGGG CGTGGGCGAC	120
CGCTTCGGGG GCGCTACGAG ACGCCGCGAC AGCTGCGGG GCGGCGCGGG ACCGCGCGGT	180
GG	182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCCGAGAG TTCTGTGAGC AGGTGCTCGA CCGAAAGTC TGGGCGCGTG CGAGCGGCT	60
GGCGGTTCAG GAGGCGAAGA CACGCGCTGT CGAGCTGCTG CGGCTCGTCT ACGGCGAGCA	120
GAGGTTCAGA TTGCTCCGCG CGGCGAGCG GATGCAAAAC TTGTGCGGCT GCATGCTCAT	180
GAGACTCGGC GATTAGGCAT TGACCAATGC GTGTACCGCG TCGCGAGCGA TTTCGAGGCT	240
CGGTTCGAG ACGAGTGGCT CGAAGCGCTT CACCGGTGAG GCGGTACGTC ATCGACACCC	300
ACGTTTGG	308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGCAGCGCGA CGAGCTCAGC TGATGATGTC TCGGCGCGCG CATTCAGGAG GGAGAGATC	60
CGGCGGAGCG TCGGCGCGCG CAGGTGCTCA TAGTGTGTCG GATAGAGGAG CTCGCGCGAT	120
GGCAGCGGAC TATTCTATTC TCGGCTGCGC CGGTAAAGAG GGTAAAGAGA ATGTGAGGGG	180
ACAGATGAGC CATTCACAGC TACGAGTGA TCGAGATGCT CGGAGCTGCG CCGGACGCGG	240
TGGAGCGCGC ATTCAGGCGG GGTCTG	267

(2) INFORMATION FOR SEQ ID NO:32:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCTCTGCCGA	AAAGATTGTA	GGGAGACGA	TGACCAATCA	CACCTACCGA	GTGATCGAGA	68
TGCTGGGAC	CTGCGCCGAC	GGCTGTGAGC	CAGCAATCCA	GGCGGGCTG	GGCUGAGCTG	128
CGACAGCAT	GGGACAGCTG	GACTGATTGC	AATACAGTTC	AATTGAGGCG	CACCTGGTGG	188
AGGAGAGCT	CGGCGCTTC	CAGGTGACTA	TGAAAGTCCG	CTTCCGCTGG	AGGATTCTCG	248
AACTTCAAG	CGCGCGCAT	AAGTAGCTG	CATCATTAAG	CGACTTTTCC	AGACATTCCT	308
GGCGGGCTG	AAACGCGCTT	CAGCGGACAG	TGGCTGCGCG	CAGCGGCTGC	CTCGAAAAATC	368
CTTGGACAA	TTCTCTGGCG	GGCGCTACAA	GGAGTGGCT	GTGCAATTTC	TGGGTATCTT	428
GGTCAGCTG	TGTGGGCTGC	AAGCGGACGA	AGCGGTGCTC	GACCTCGGCT	GCGCTTCGGG	488
GGGATGGCG	TTGGCGCTCA	CGGGCTATCT	GAACAGGAGG	GGACGCTAGG	CGGCTTCCGA	548
TATCTGCCAG	AAAGCTCTCG	GGTGTGGCA	GGAGACATG	AGTGGCGCG	AGGCAACTTT	608
CGAGTTGGAG	GTCTCCGACG	TGTACAATCG	GCTGTACAA	CGGAAGGGGA	AATACAGTTC	668
ACTAGACTTT	CGTTTTCGAT	ATCGGAGTGC	GTGGTTGGAT	GTGGTGTTC	TTAGCTGGGT	728
GTTCAGCGAG	ATGTTTCCGC	CGGACGTGGA	GCATTTCTTG	GACGAGATCT	CCGCGGTGCT	788
GAAGCTCGCG	GGACGATGCG	TGTGCGGTA	CTCTTTGCTC	AATGACGAGT	GCTTAGCGCCA	848
CTTCCGGGAA	GGAAAGAGTG	GACACAGCTT	CGAGCATGAG	GGACCGGCTT	ATCGGACAAAT	908
CGACAGAGAG	CGGCGCGAGG	AGGCAATGCG	CTTTCGCGAG	AGCTTGTGCA	GGATTTGCTA	968
TGGCACTTTC	GGCTCTCGCG	TGAGCGAGCG	ATTGCGCTAC	GGCTCATGGA	GTGGCGCGGA	1028
ACGACGCGCA	AGCTTTCGAG	ACATCTGCTT	CGGACGAGAA	AGCGGAGCTT	AGTTGGGCTT	1088
GGGGAAGGCA	TGGGACATCC	GTGAGGCTGA	GGGCTGTGCG	CGGAGGCGCG	ATTAGTGGGG	1148
CAGATTAGCG	CGGCGCGGCT	CGGCTCTGCG	AGTAGGCGCG	CCGCAATGCG	GTACCGGCGT	1208
GGTAAGCAGG	CTTGGCGGCG	TGGCGGCGCG	CTTGGCGGAT	CAGCTGTGAG	ATGGCGACAA	1268

AGCCTGCGTG ATCGGTGATC ACCAAGGGTG ACAGGAGCGG ATTGTGCACC AGCGGGAGCG	1320
CGACCGCGGT CTCCGGGTGT GTCCAGCGGA TCAGCGCGCG CAAGCGCACA TGACCAAGCC	1380
CGGCGATCAC GTTGGCGATG GCGATACGCT GATAGCCAAG ATGAAATATT AAGGGCAGCA	1440
ATAGATTTCG ATCGGGCAGA ACITGCGGTC GGTTCGGGCT CAGGCGCGTG ACCAGCTGCC	1500
GGGACAAGAA GGTATGCGCG TGATCTCGCG CTGCTGCGG	1539

(7) INFORMATION FOR SEQ ID NO:33:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGAGGGGTA GGTGGGATGA GGTGACCGCG GGGCGAGGCG GAGCTGACCG CGCGCGAGGT	80
CAGGTTTGCT GCGCGGGCTT ACAGACGGCG GTATGGGCTG AGGTGCGCCC CGCGGTTGAT	120
CGCGGAGAGC CTTCTGAAC TGATGATTCT GATAGCGACC AGCTCTTTGG GCGAAGACAC	180
CGCGCGGATC GCGGTGACCG AAGCGGAATA CGGCGGATG TCGGCGCAAG AGCGCGCGCG	240
GATGTTTGGC TACGCGCGCG CGCGCGCGCG GCGGAGGCG AGTTGCTGCG GTTTCAGGAA	300
GGCGCGGAGC ATGACCGGCG CGGTGGGCT GTTCGAGCGG GCGGCGCGCG TCGAGGAGCG	360
CTCGGACGCG GCGCGCGGCA ACCAGTTGAT GAGCATGTC CGCGGCGCG TGAACAGATT	420
GCGCGGCGCG AGCGGCGCA TCAGCGCTTC TTTCAGGCTG GGTGCGCTGT GGAAGACGGT	480
CTCGGCGGCT GGGGTGCGCA TGAGCAACAT GGTGTGAGCG GCGCAAGACG AGATGTGAT	540
GACGAGTCTG GGTGTGTGCA TGAGCAACCG GTTCAGCTCG ATGTTGAGCG GCTTTGCTCG	600
GGCGCGGCGCG GCGGAGCGCG TGCAACCTGC GCGCAAAAC GGGGTGCGCG CGATGAGCTC	660
GCTGGGCGCG TCGGTGAGTT CTTCGAGCTC GGGCGCTGGG ATGCGCGCGC AGTTGGGCTC	720
GGCGCGGCTCG GTACGGATG GTACCGCGCA TGCGGGAATA TACGAGAGT CTGGTGGCGC	780
GAAGGCTGCT GCGGCGTAAG GTTACGCGCG GTTTCCTGGA TCGGCTGAAC TTGCTGAAC	840
GAACAGCTTA C	851

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGTCGG	CCGGAATT	GGCCAGATT	CCCTCCGGC	GATAACCAA	TCAATCGAAG	60
CTAGATTAT	TCCGTCAGG	GGCCGAGTA	ATGGCTCGA	GGAGAGGAG	CTTACTGCTG	120
GGGCGAGTA	TCTAGGTC	TGATAGGCG	GGAGGAGTC	GATTTTTC	AAGGACAGCC	180
CAATCGAAG	CTTCAGGCG	CACTCCAGT	TCTGAGCGG	GGAGGCACT	CCGAGGCTGC	240
GCTTCGCA	GATC					254

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCTGAGC	GAAGCGGCG	CGCCAGGCG	CAAGTCGCTG	TTGAGGAGG	AGGACGGGA	60
CAATCTGCG	CTCGGATCG	CGTTTCAGC	GGAGGGTTC	CTTGATTCG	GTATACCTT	120
TTTCTGAGC	GACCGAGCG	TGATGCTGA	CGAACCGCG	CAATCGGTC	GTCTCAGGT	180
ATCTCTGAG	CGATGAGCG	CGGATATCT	GGAGGGTTC	TGATGATTT	TGCTGAGAG	240
TATTCGAGG	CAAGTTTCG	CATGAGGAT	CGGAGGCGA	CGGCTCTCG	CGGCTGCGG	300
GATTCGTTA	ACTGATAAA	CGTAGTACG	ATTCGCGCT	CGGAGAGCG	TAGGAGGAG	360
CGAGAGGCG	ACCGGCTCG	AGAGGAGCT	GAGGATTCG	TTGAGGCTA	CGGCTGCGG	420
GGCGGCGCG	GGAGGCTTC	AGTTCAGTC	TGAGAGGAG	CTGGGCTGA	TATTCGAGG	480
ATGAGGAGG	TTTCTGAGC	GAGTCTGCT	CGAGTTCGA	GAGTCTGCT	CGGAGGCTT	540

CGCTGCTGAG CTTCGGCAAG GCTGATCGG AGCGCTTGTG GCGCAGCGCG TCGTGGATAC	680
GCGCAGCGCG ATTCCGAACG ATGCTGTGTA CTTCCGGTT CTCCAGCGCG TTGAGGTATC	690
CCTGATCGG GCTTTTCGGG GGTCCCTCG AGAATCTGCC TCGCTGTTC GCTCGCTTGG	720
TGCGGACGCG GTATATGATC GCGCGCTCA TAGCGACAC CAGCGCGAGC GGTACCGCAA	750
TGCTGATGAG CAGCCGCTTC TCGCTCGCT TCGGTAGGA CAGCTCGCG GGTACCGCG	840
GATATCGCG GCGCGCGCG GCGCGCTGT CTGCGCTTC CCGCGCGAG GCGCTTTCG	900
CGCGCGCGAG GTCTGGGCG TAGTCCAGCG CTTCGCGTTC GTGGGATGAG GGTCTGGGCT	960
AGCGCGCGCG TCGCTTCTG CCGACAGCG GCTTCGCGCA GTGGGACCG GGTATTCTCG	1020
TTCTCTAGG CTGCTGAGC GACCGAGCT CTGCGCGCG CAGCGCGCT GCGCTCGCG	1080
GCGCGCTTC GCAATCAGT GAGCTCTCT GCGAGGTAG CGCAGCGCT GCGCTGCTTC	1140
CTCAGCGCG CCGCGCGCG GCGCGCGCG ATATCTTTC AAGCTAGCG AACCTAGGA	1200
ACGAGCGCG GAGATTCTCT GAGGATC	1227

(2) INFORMATION FOR SEQ ID NO:36:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 181 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(1) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGCTGCTGAG CCGATCGCG GGTGCTTTC AGCGCAGCG CCGCGCGCG GCGCGCGCG	60
GCGCGCGCG TAGCGCTTC GCGCGCGCG AGCGCTTCT CTTCGCGCG GCGCGCTTC	120
GCGCGCGCG CAGCAATCT GCGCGCGCG GCTCGCGCG ATTCTCTAC GCGCGCGCG	180
G	181

(2) INFORMATION FOR SEQ ID NO:37:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGGTGTCTG	CGGATCCGGC	GGGTGGTTTA	ACGGCAACGG	CGGTGTCTGG	GGCGGGGGCG	60
GGAGAGGCGT	CTTTGCGGCT	GCGGGCGGCT	AGGGCGGCGT	CGGTGGTCAG	GGCGGCAATG	120
GGGGGGGCTC	CACGCGCGGC	AACTGGCGTC	TTGGCGGGCG	GGGGGGTGGC	GGAGGGGAACG	180
CCCCGGAGCG	CGGCTTCGGT	GCGACCGCGG	GTAAGGGTGG	CCAGGGGGCG	ATTGCCGGCG	240
GGACTCAGAG	CGCGACGGCG	CTCGGCGGTC	ACGGCGGTGA	CGCGGGTGA		300

(2) INFORMATION FOR SEQ ID NO:38:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCGACTGG	CATGGGGGGT	CTCAGTGGAA	GGAT	34
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(2) INFORMATION FOR SEQ ID NO:39:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGCTGCT	GATGCCCCCG	TTGGCGCGCG	GGCACCGGCT	CCGACGGTTA	CGGAACCAAC	60
TGGCGTGGTC	GGCAGACACX	CGGGGCGCGG	CGGGGGGGCG	GTGGACAAAT	GGCACCGTGT	120
TATCGGACAC	ATTGCGGXXG	GGCGGACGGG	CACCG			155

(2) INFORMATION FOR SEQ ID NO:40:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGAGTTCA GCGCGGCCG GAGACCGGC AGCCCGGNG GCGCGGGGG TGG 53

(2) INFORMATION FOR SEQ ID NO:41:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCACCCC GGTGCGNAG GGTGCGGCG GGGCCACCC GAGCAGGGC GGTAAAGGG 68

GCACCGGCG CAACGGGCG ANDGCAAG TGTGCGGNG GCGCGGCGG CCGCGCGGA 126

AGGCGGCAA CG 132

(2) INFORMATION FOR SEQ ID NO:42:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGGCG CGGACGAGG GGGGCGGCG GCGAGGGCG NAACGGGGG GCGGAGCCA 60

CAGCGCAAG ATCTCTCGG TGCTCATAT GCGCGAATG GAGCAGGGC GCGACGGCG 120

GCAGGGCGG CA 132

(2) INFORMATION FOR SEQ ID NO:43:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 767 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

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CGGACAGGAG ATCGGTACCC GCGCGCATG GACGCTGCG ATTCGCGGGG TTGGGCGACC      60
CGACGAAAGC GCGTACGAG TGGGCTGCG GAAGTAGGCG GATCGCTTCG CGATGCGCGC      120
ATGAACGGCG GCGATCAAA TATGCGAGG ACCTTCAGT TTAGCGACGA TAATGCGTAT      180
ACCACTAAGG AGGATGATCC GATATGAGC AGTCGCGAG CGTGACGGTC GATCAGCAAG      240
ACATTTTGA CCGGCGCAG GAGGTGAGG CCGCGATGCG CGAGGCGCGC ACTGATGTCC      300
CGATCAGACG GTGCGAGTC ACCTGGGTA AAAACGCGC CCAAGAGTC GTTTTGTCCG      360
CGGCGACAT GCGCGAATAC CTGCGGCGCG GTGCGAAGA CGGCGAGCTT CTGGCGAAGT      420
CGCTGCGGAA CCGCGCAAG GGTATGCGC AGCTTGATGA CGAGCTGCG AGCGCGCTGG      480
ACAGCGGCGC CGAAGGAGT GTGAGGCGG AATCGGCTCG GCGCTGTGGA GCGGACGATT      540
CGCG/GAGCT AACGATAGC CGAGGCTCG CAGCGCGCG TGAACCGAC TTCATGGATC      600
TGAAAGGAGC GCGAGGAGG CTGAGAGCG GCGACGAGG GCGCTGCTC GCGGACTGCG      660
GGGATGGGTC GACACTTTC ACCCTGAGCG TGCAAGCGGA CG                                702

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(12) INFORMATION FOR SEQ ID NO:44:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 298 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

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GAAGCGCGCG GCGTGCAGG CGAATTCGCG CTCGAGGCG CATCGCTGCG TGGGGTGGG      60
GGGGGCGCGG TGGGCTGCG GCCCTTGGG TCGCGGATCG GCGCGCGGGA ATCGGTGCGG      120
CGGCTGCGCG CTGATGAGT TCGCGGCTTA GCGCAGGGA GCGCGGCGCG GCGCGCGCGG      180

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CTGGGGGGGG GTGACATGGG AATGCCGATG GGTGCTCGGC ATCAGGGAGA AGGGGGGGCC	240
AAGTCCAGG GTTCTCAGCA GGAAGAGAG GGGCTCTAGA CCGAGGATCC TCGTGCGG	298

(2) INFORMATION FOR SEQ ID NO:45:

(A) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(E) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG ATGATATCGG GTGXXGCGG ACACAGGCTC GCACTCGACC AGTGGAGGAG	60
CGATGACCTA CTGTCXXGGT AACCCGAGAT ACCCGCAGG CGAGCCCGCA GGTTCCTAGC	120
GAGGCTGAC AGCTCTGTC GCCACGCGG ATGAGGAGTC GAGCAAGCTA CGATGTATCC	180
TGACATCTGC GTTGGCACTG CTGXXCTGCG CTGCTACTTT GCGGAGCTT GCCCAATGT	240
TCACCTCTAG TACCGAATCG GGGGCGGCTG ATGGGCGAGT GTCCGCTGAC ACTGGGCTGC	300
CGCTCGGGGT GACTCTGCTG GCTGGGATCC TTGCGTGGGT GGTTCCTGCT CCGTAGGCCA	360
AGAGCATGCT GACCGTAGTT GCGCTGCTCG GGTACTCGAG CGTATTCTCG ATGCTCTCGG	420
CGACCTTTAA CAAGTCCAGG GCGTATCTGA CGGCTGCGC ATTGTGAGTT GTGTTCCTTT	480
TTATCTGTTT CGAGGCGGTT CGGCGAGTTC TGAGGCTCTT GGTGGAGGAC GCGGCTATCA	540
CGGCTCTGCG GCGCGAGTTC AAGTTCAGCC CGTATGAGCA GACCGGCGCC TACGCGCACT	600
ACGGCAGATG CGGCGTCCAG GGGGTGGGTT ACTACGCTCA GAGAGGCTCT CAACGAGCGG	660
CGGCACTGCA GTGGGCGGCG GCGGCGCACT CTGCGCAGCC TCGCGGATAT GGTTCGCAAT	720
ACGGGCGCTA TTGCTCGAAT CGGAGCGCAAT CGGCGAGTGG ATAGACTGCT CAAGCTCTCG	780
CGGCGCGGCG GCGCGAGTCC GGGTGGCAAC AATCGACCTA GCGGCGATCC AGCGCACCTA	840
CGGCTCTTCC GAGCTTCAGC CCAGCGCGAC GAGTCTAGTC CGGAGCGGCG TCGCGAGCTG	900
GTTCGGCTTC ACTCAACTAT TCAGAGCGCA GGGGAGGCGA GCACTGCTCG TCGCGCGGCG	960
GCGCGCGGCT CTAGCGCGGG GTTCGCGGCT CGGTCGCGCG GTGTCGCGGA AGAGTGAACA	1020
GGGTGTGAGC AAGCGCGGAC GATCGTCTGT CCGAATTC	1058

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCGACGAG	GACCGATGCG	CGTACCTCTG	CGCAGGAGCG	AGGTATTTC	GACCGGATCT	60
CGCGGACCT	GAAACCCAG	ATCGACGACG	TGGAGTGAC	GCGAGCTTCG	TTGAGGGGCG	120
AGTGGCGCG	CGCGCGCGCG	AGGTCCGCT	AGGCGCGCT	CGTGGCTTC	CGAGAGCGAG	180
CGATTAGCG	GAGCGAGAA	CTGACGAG	TCTGACGGA	TATTCGTCA	GCGGGCTTC	240
AATACTGAG	GCGGACGAG	GAGCGAGCG	AGGCGCTTC	CTGCAAGT	GCTTCTGAC	300
CGCTATTAC	GAAAGAAAG	GCGCGAG				327

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTCCGAT	GATGGCTTC	TGCAACCTGA	CGATTCTCT	ACGCGCTCG	TTGAGATCA	60
CGAACAAGT	TTTGGCTTC	GCAATCTCG	CGACCGCTG	GATCTGGTG	ATCTTCTCT	120
TCTTATCAG	GAGTGCAGA	CGGCTACCT	TGCTCGAG	TACCTTTCG		170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGC	CACCGGGGT	GGCGGGGCA	GCACGGTGG	CGCTGGGGG	ACGGGGGGG	60
CCGGGGTGG	CGGGGGGAC	GGGGGGTGG	TCTGGGGAA	CGGGGGTGG	GGGGGGGAC	120
GGGGGGT						127

(2) INFORMATION FOR SEQ ID NO:48:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGCGGGGAA	GGGGGGGG	CGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	60
CGCGGGGTC	GGGGGGGAC					91

(2) INFORMATION FOR SEQ ID NO:49:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCAGGGGT	GGGGGGGT	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	60
GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	120
GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	149

(2) INFORMATION FOR SEQ ID NO:51:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(1) TOPOLOGY: linear

(ix1) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGUCACGAGA TCACCCCTAC CGACTGATCG AGATCTGCGG GACCTGGCCC GACGGTGTCC	60
ACCGCGAAT CCAGCGCGGT CTGGCTCCAG CTGGCGAGAG CATGGGCGCG CTGGACTGGT	120
TCGAGGTACA GTCAATTGCA GCGGACCTGG TCGACGGAGC GGTCGCGGAC TTCCAGGTGA	180
CTATCAAAAT GGGCTTCCGC CTGGAGATT CTTGAAATTT CAAGCGCGCG CGATAACTCA	240
GGTGATCATT TAAGCGACTT TTGAGAGAC TCTGACCGCG CTGGAACGCG GGTTCAGCGG	300
ACGGTGGCTC CGCGGAGCGG CTGCTCTCAA AATGCTTCCG ACATTTCTCT GCGCG	355

(2) INFORMATION FOR SEQ ID NO:52:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix1) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGATCAAC ATCCCATCA CATGCATCA GTGACCCCA ACTTGACAG TCGAAAGCA	60
CGATTGGGCG GACTGGCTAT CCGGCGATG GCGAGCGCG GCTTGATGAC GGTTCGGTTC	120
CGCGGCGCG CCAAGCGCTA TCGGAGCCA CGGCGCTCGG TACCGACAC GCGCGCTTCG	180
CGCGGCTGCA CGCTTCAGG GTCAGCGCA CGGCGACAC CTGTTGCTCC CAGATCAGCG	240
GGCGCGGCA AGACGGCGAA TCGGAGCGG GCGATCCCA AGCGAGCAG TCGCGGGGCT	300
GACTCGAGCG CAGCGCGCG ACTGTCATT GCGCGAAGC CAGCGCAGC TGTGCGGCTC	360
GCGAGCGCG TTGAGAGAT GAGCTTCCCG CTGCTGCTG GTCGGTGGG CTCTGAGCGC	420
GCTGCTCTCG ACTAGCTTC AGCACTGCTG AGCAAAAGA CGGCGAGCG GGCATTTCCT	480
GGACGCGCGG CGCGCTTGG CAATGAGAG CATTATGTC TCGCGCTGCT AGACCAAAAG	540
CTTTACGCGG GCGCGAAGC CAGCGACTCG AAGCGCGCG CGCGCTTGGG CTGCGACATG	600
GCTGAGTCTT ATATGCGCTA CGCGGCGAG CCGATCAAGC AGGAAAGCTT CTGCTGAGAC	660

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GCCAGGGG TGTCTGGAAG CGGCTGCTAT TACGAAGTCA AGTTCAGGCA TCCGAGTAG 720
CCGACGGGCG AGATCTGGAG CGGCTGATTC GACTGCGGCG CGGCGAGGCG AGGGGAGCG 780
GGGGCCCCC AGGCGCTGCT TGTGATATG CTGCGGAGCG CCGACGACCG GATGGACAG 840
GGGGAGGCGA AGGGGCTGGC CGATCGATC CCGGCTTGG TGGGCGGCGC CGGGGCGCG 900
CGACCGGCTC CTGGAGAGCG CCGTCCGCGC CGGCGCGGCG CGGGGAGAGT GAGTCTTACC 960
CCGAGGACAC CGACAGCGCA GGGGAGCTTA CCGGCTGA 999

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(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: Linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1           5           10           15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20           25           30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35           40           45

Gln Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50           55           60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65           70           75           80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85           90           95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100          105          110

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115          120          125

Phe Ala Leu Pro Ala Gly Trp Val Gln Ser Asp Ala Ala His Phe Asp
130          135          140

Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro

```


(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Gln	Ala	Ala	Lys
1			5					10							15

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1			5					10						15

(2) INFORMATION FOR SEQ ID NO:58:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp	Ile	Gly	Ser	Glu	Ser	Thr	Glu	Asp	Gln	Gln	Asn	Ala	Val
1				5								10	

(2) INFORMATION FOR SEQ ID NO:59:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala	Gln	Gln	Ser	Ile	Ser	Thr	Asn	Gln	Asn	Ile	Val	Pro
1				5								10

(2) INFORMATION FOR SEQ ID NO:60:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp	Pro	Gln	Pro	Ala	Pro	Pro	Val	Pro	Thr	Ala	Ala	Ala	Ala	Pro	Pro
1				5						10				15	

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

141 SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Ala Pro Lys Thr Tyr Ser Glu Gln Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

III. SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
```

[8.4] EXPERIENCE DESCRIPTION: SEP ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Cln Cln Thr Ser
 1 5 10 15
 Leu Leu Asp Asn Leu Ala Asp Pro Asp Val Ser Thr Ala Asp
 20 25 30

2. INFORMATION FOR THE USER

(1) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
```

(44) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Gly Cys Gly Asp Arg Ser Gly Gly Asn Leu Asp Gln Ile Arg Leu Arg
1 5 10 15
Arg Asp Arg Ser Gly Gly Asn Leu
20

(2) INFORMATION FOR SEQ ID NO:64:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(a) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Thr Gly Ser Leu Asn Glu Thr Ala Asn Arg Arg Ala Asn Glu Arg Lys
 1             3             10             15

Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
 20             25             30

Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35             40             45

Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
 50             55             60

Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
 65             70             75             80

Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
 85             90             95

Asn Lys Gly Ser Leu Val Gln Gly Gly Ile Gly Gly Thr Glu Ala Arg
100             105             110

Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
115             120             125

Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
130             135             140

Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
145             150             155             160

Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
165             170             175

Ser Ala Met Gln Leu Leu Gln Ala Ala Gly Asn
180             185

```

(2) INFORMATION FOR SEQ ID NO:65:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
1           5           10           15
Ser Glu Leu Asp Ala Pro Ala Glu Ala Gly Thr Glu Ser Ala Val Ser
20           25           30
Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
35           40           45
Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Glu Ala Ile Thr Ser
50           55           60
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
65           70           75           80
Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
85           90           95
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
100          105          110
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Glu Ile Gly Lys Leu
115          120          125
Arg Leu Val Phe Leu Thr Gly Pro Lys Glu Gly Glu Asp Asp Gly Ser
130          135          140
Thr Gly Gly Pro
145

```

(2) INFORMATION FOR SEQ ID NO:66:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1           5           10           15

```

Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
 20 25 30
 Gln Arg Asp Ala Leu Cys Leu Ser Thr Gln Ile Ser Arg Gln Ser
 35 40 45
 Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
 50 55 60
 Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
 65 70 75 80
 Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu
 85 90 95
 Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
 100 105 110
 Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
 115 120 125
 Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
 130 135 140
 Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn
 145 150 155 160
 Ile Thr Ser Ala Phe Tyr Glu Ser Ala Ile Pro Pro Arg Gly Thr Gln
 165 170 175
 Ala Val Val Leu Asn Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
 180 185 190
 Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
 195 200 205
 Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
 210 215 220
 Phe Pro Ile Val Ala Arg
 225 230

(2) INFORMATION FOR SEQ ID NO:67:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acids
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(21) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20           25           30

Gly Gly Gly Ser Pro Thr Val His Ile Qly Pro Thr Ala Phe Leu Gly
35           40           45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly His Arg Val Gln Arg Val
50           55           60

Val Gly Ser Ala Pro His Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65           70           75           80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85           90           95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100          105          110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115          120          125

Gly Pro Pro Ala
130

```

(3) INFORMATION FOR SEQ ID NO:68:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(21) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1           5           10           15

Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro
20           25           30

Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35           40           45

Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Asa
50           55           60

```

```

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65              70              75              80

Ile Glu Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85              90              95

Ser Glu Arg Lys
100

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1              5              10              15

Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20              25              30

Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Arg Asp
35              40              45

Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50              55              60

Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65              70              75              80

Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85              90              95

Arg Arg Gly His Arg Arg Ala Asn Thr Gly Ala Val Leu Arg His Pro
100              105              110

Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115              120              125

Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130              135              140

His Arg Xaa Gly Pro Val Asp Gln Pro Asp Arg Arg Leu Pro Val Arg
145              150              155              160

Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
 1           5           10           15

Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20           25           30

Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35           40           45

Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Glu Val Pro
50           55           60

Arg Gly Arg Lys Glu Ala Val Ala Ala Ala Val Ala Ala Ser Leu Arg
65           70           75           80

Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
85           90           95

Glu Thr Asp Thr Ala Ala Ala Leu Leu Ala Gly Thr Ala Pro Ala Ala
100          105          110

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
115          120          125

Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
130          135          140

Leu Gly Thr Ala Val Glu Phe His Phe Ile Ala Arg Leu Val Leu Val
145          150          155          160

Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Glu Glu Leu
165          170          175

Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
180          185          190

Ala Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
195          200          205

Asp Arg Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Thr

```

210	215	220
Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro		
225	230	235 240
Thr Arg Glu Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro		
	245	250 255
Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro		
	260	265 270
Ala Asp Leu His His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala		
	275	280 285
Pro His Glu Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu		
	290	295 300
Arg Thr Asp His Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr		
305	310	315 320
Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Glu		
	325	330 335
Val Ser Arg Glu Asn Pro Thr Gly		
	340	

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala		
1	5	10 15
Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Glu Asp Cys Val Glu		
	20	25 30
Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile		
	35	40 45
Ile Tyr Arg Glu Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu		
	50	55 60
Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Val Thr Val Leu		
65	70	75 80

Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85 90 93
 Thr Gly Glu Leu Met Arg Arg Ser Ala Arg Cys Val Ala Ala Ala Glu
 100 105 110
 Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
 115 120 125
 Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
 130 135 140
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
 145 150 155 160
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Glu Ala Ala
 165 170 175
 Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
 180 185 190
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
 195 200 205
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
 210 215 220
 Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
 225 230 235 240
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
 245 250 255
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
 260 265 270
 Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
 275 280 285
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Arg

370	375	380
Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Gln Leu Gly Gln Ala		
385	390	395
Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Gln		
405	410	415
Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Gln Gln Ala Val Arg		
420	425	430
Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala		
435	440	445
Ser Arg Arg Leu Ala Gln Gln Arg Gly Ala Phe Pro Ala Phe Thr Asp		
450	455	460
Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser		
465	470	475
Val Ala Pro Thr Gly		
485		

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Val Ile Val Leu Asp Leu Gln Pro Arg Gly Pro Leu Pro Thr Gln	
1	15
Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val	
20	35
Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala	
35	45
Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His	
50	60
Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Gln	
65	80
Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Gln Thr Pro	
85	95


```

Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
      106                      125          110

Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
      115                      120          125

Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
      130                      135          140

Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
      145                      150          155

Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
      165                      170          175

Cys Ala Pro Ser Asn Gln Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
      180                      185          190

Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
      195                      200          205

Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
      210                      215          220

Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
      225                      230          235          240

Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
      245                      250          255

Ala Pro Pro Pro Gln Ser Pro Ala Gln Gly Gly
      260                      265

```

(2) INFORMATION FOR SEQ ID NO:73:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1           5           10           15

Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
20          25          30

Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
35          40          45

```

```

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50          55          60
Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65          70          75          80
Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
 85          90          95
Gln

```

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 364 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1          5          10          15
Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20          25
Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Gly Ser
 35          40          45
Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50          55          60
Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65          70          75          80
Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
 85          90          95
Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
100          105          110
Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro His Ala
115          120          125
His Thr Tyr Asn Ile Lys Gly Val Gln Thr Leu Asn Leu Asp Gly Pro
130          135          140
Thr Thr Ala Lys His Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro

```

148	150	155	160
Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile			
	155	170	175
Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln			
	180	185	190
Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser			
	195	200	205
Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly			
	210	215	220
Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu			
	225	230	235
Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr			
	240	245	250
Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys			
	255	260	265
Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu			
	270	275	280
Asp Thr Ser Ser Phe Tyr Arg Pro Thr Glu Pro Gly Ser Tyr Pro Ile			
	285	290	295
Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr			
	300	305	310
Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly			
	315	320	325
Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe			
	330	335	340
Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser			
	345	350	

(2) INFORMATION FOR SEQ ID NO:75:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(a1) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Gln Asp
 1 5 16 15
 Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
 20 25 30
 Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
 35 40 45
 Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
 50 55 60
 Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
 65 70 75 80
 Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Gln His Pro
 85 90 95
 Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
 100 105 110
 Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
 115 120 125
 Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
 130 135 140
 Gln His Arg Gly Gly Pro Val Thr Val Arg Arg Val Pro Gly Val Arg
 145 150 155 160
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
 165 170 175
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
 180 185 190
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
 195 200 205
 Pro Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
 210 215 220
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
 225 230 235 240
 Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg
 245 250 255
 Arg Ala Gly Gly Ala Gln Arg Ala Asp Pro Gly Gln Arg Gly Arg His
 260 265 270
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr
 275 280 285
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg

290

295

300

Asn Arg Pro Arg Arg

305

(x) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 580 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1           5           10           15
Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20           25           30
Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35           40           45
Ser Pro Leu Gln Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50           55           60
Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65           70           75           80
Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser
 85           90           95
Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Gln Ser His Thr His
100           105           110
Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln
115           120           125
Glu Gln Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
130           135           140
Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Thr
145           150           155           160
Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln
165           170           175
Pro Thr Gln Tyr Arg Gln Pro Tyr Gln Ala Leu Gly Gly Thr Arg Pro
180           185           190

```

Gly Leu Ile Pro Gly Val Ala Pro Thr Met Thr Pro Pro Pro Gly Met
 195 200 205
 Val Arg Glu Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val
 225 230 235 240
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270
 Glu Glu Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285
 Asp Leu Gly Asn Glu Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Lys
 305 310 315 320
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
 325 330 335
 Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp
 340 345 350
 Ile Ala Val Val Arg Val Glu Gly Val Ser Gly Leu Thr Pro Ile Ser
 355 360 365
 Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Glu Pro Val Leu Ala Ile
 370 375 380
 Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser
 385 390 395 400
 Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Glu Asn
 405 410 415
 Thr Val Leu Asp Ala Ile Glu Thr Asp Ala Ala Ile Asn Pro Gly Asn
 420 425 430
 Ser Gly Gly Ala Leu Val Asn Met Asn Ala Glu Leu Val Gly Val Asn
 435 440 445
 Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Glu Ser Gly
 450 455 460
 Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Glu Ala Lys Arg Ile
 465 470 475 480
 Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly

	485		490		495
Val Glu Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu					
500		505		510	
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val					
515		520		525	
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu					
530		535		540	
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr					
545		550		555	
Phe Glu Asp Pro Ser Gly Gly Ser Arg Thr Val Glu Val Thr Leu Gly					
560		565		570	
Lys Ala Glu Glu					
580					

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu			
1	5	10	15
Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro			
20	25	30	
Asp Ala Glu Glu Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro			
35	40	45	
Ala Leu Leu Ala Glu Phe Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu			
50	55	60	
Thr Ser Val Ala Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu			
65	70	75	80
Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala			
85	90	95	
Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Glu Gly Val Pro Phe Arg			
100	105	110	

114

```

Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
    115              120              125

Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
    130              135              140

Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
    145              150              155              160

Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
    165              170              175

Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
    180              185              190

Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
    195              200              205

Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
    210              215              220

Lys Trp Asn Gln Pro Val Asn Val Asp
    225              230

```

(7) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Val Ile Asp Ile Val Gly Thr Ser Pro Thr Ser Trp Gln Gln Ala Ala
1              5              10              15

Ala Gln Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
20              25              30

Ala Arg Val Ile Gln Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
35              40              45

Thr Tyr Arg Ile Lys Leu Gln Val Ser Phe Lys Met Arg Pro Ala Gln
50              55              60

Pro Arg
65

```

(2) INFORMATION FOR SEQ ID NO:79:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(4d) SOURCE DESCRIPTION: SFO ID NO. 79.

```

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
1      5      10      15
Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
20      25      30
Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Thr Pro Pro Ala Pro Pro
35      40      45
Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
50      55      60
Ser Pro Pro Leu Pro
65

```

121 INFORMATION FOR SDO TO HQ: HQ.

2.2.1. SIGNIFICANCE OF THE CONCEPT

- (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(X) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met	Sec	Arg	Sec	Arg	Arg	Arg	Sec	Leu	Arg	Thr	Sec	Trp	Leu	Leu	Sec
1			1						10					15	
Val	Leu	Ala		Val	Gly	Leu	Gly	Leu	Ala	Thr	Ala	Pro	Ala	Gln	Ala
		20						25					30		
Ala	Pro	Pro	Ala	Leu	Sec	Gln	Asp	Arg	Phe	Ala	Asp	Phe	Pro	Ala	Leu
		35					40					45			
Pro	Leu	Asp	Pro	Sec	Ala	Met	Val	Ala	Gln	Val	Ala	Pro	Gln	Val	Val
		50				55					60				
Asn	Gln	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn	Ala	Val	Gly	Ala	Gly	Thr
65				70						75				80	

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Glu Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Gln Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Glu Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Glu Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met His Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

Ser Pro Lys Pro Asp Ala Glu Glu Glu Gly Val Pro Val Ser Pro Thr
  1          5          10          15

Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Glu Ser Leu Asp Ala
  20          25          30

Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
  35          40          45

Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
  50          55          60

Arg Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Glu Gly
  65          70          75          80

Val Pro Phe Arg Val Glu Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
  85          90          95

Asp Tyr Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val
  100          105          110

Leu Asp Phe Ala Ala Gly Val Thr Glu Leu Leu Ser Gly Val Thr Asn
  115          120          125

Leu Glu Ala Glu Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys
  130          135          140

Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
  145          150          155          160

Ala Lys Ser Ala Arg Pro Ala Thr Val Tyr Ile Ala Glu Asp Gly Ser
  165          170          175

His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Glu
  180          185          190

Leu Thr Glu Ser Lys Trp Asn Glu Pro Val Asn Val Asp
  195          200          205

```

(2) INFORMATION FOR SEQ ID NO:82:

(ii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1             5             10             15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
20             25             30

Ala Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
35             40             45

Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
50             55             60

Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
65             70             75             80

Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
85             90             95

Asn Phe Asp Pro Gln Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
100            105            110

Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
115            120            125

Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Gln Trp
130            135            140

Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
145            150            155            160

Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
165            170            175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
180            185            190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
195            200            205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
210            215            220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp

```

225	230	235	240
Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg			
245	250	255	
Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln			
260	265	270	
Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Asn Lys			
275	280	285	

(12) INFORMATION FOR SEQ ID NO:81:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (R) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr		
1	5	10
Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp		
20	25	30
Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Asn		
35	40	45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg		
50	55	60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Glu Phe Asp Arg Pro		
65	70	75
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Gln Arg Thr Val Thr Asp		
85	90	95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu		
100	105	110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Glu Ile Glu Glu Val		
115	120	125
Ala Leu Met His Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn		
130	135	140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro		
145	150	155
		160

Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
165 170

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser His
1 5 10 15
Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly
20 25 30
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
35 40 45
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
50 55 60
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
65 70 75 80
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Gln Gly Gly Ile
85 90 95
Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Met Gln
100 107

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
1 5 10 15
Pro Leu Gly Gln Pro Ile Asn Gly Arg Gly Asp Val Asn Ser Asp Thr

121

Arg	Arg	Ala	Leu	Gln	Leu	Gln	Ala	Pro	Ser	Val	Val	Xaa	Arg	Gln	Gly
		35					40					45			
Val	Lys	Gln	Pro	Leu	Xaa	Thr	Gly	Ile	Lys	Ala	Ile	Asp	Ala	Met	Thr
	50					55				60					
Pro	Ile	Gly	Arg	Gly	Gln	Arg	Gln	Leu	Ile	Ile	Gly	Asp	Arg	Lys	Thr
	65				70				75					80	
Gly	Lys	Asn	Arg	Arg	Leu	Cys	Arg	Thr	Pro	Ser	Ser	Asn	Gln	Arg	Glu
		85						90					95		
Glu	Leu	Gly	Val	Arg	Trp	Ile	Pro	Arg	Ser	Arg	Cys	Ala	Cys	Val	Tyr
		100					105						110		
Val	Gly	His	Arg	Ala	Arg	Arg	Gly	Thr	Tyr	His	Arg	Arg			
	115						120					125			

(2) INFORMATION FOR SEQ ID NO:86:

(A) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Cys	Asp	Ala	Val	Met	Gly	Phe	Leu	Gly	Gly	Ala	Gly	Pro	Leu	Ala	Val
1				5				10					15		
Val	Asp	Gln	Gln	Leu	Val	Thr	Arg	Val	Pro	Gln	Gly	Trp	Ser	Phe	Ala
		20					25					30			
Glu	Ala	Ala	Ala	Val	Pro	Val	Val	Phe	Leu	Thr	Ala	Trp	Tyr	Gly	Leu
	35					40					45				
Ala	Asp	Leu	Ala	Glu	Ile	Lys	Ala	Gly	Glu	Ser	Val	Leu	Ile	His	Ala
	50				55					60					
Gly	Thr	Gly	Gly	Val	Gly	Met	Ala	Ala	Val	Gln	Leu	Ala	Arg	Gln	Trp
	65				70				75				80		
Gly	Val	Glu	Val	Phe	Val	Thr	Ala	Ser	Arg	Gly	Lys	Trp	Asp	Thr	Leu
		85						90					95		
Arg	Ala	Xaa	Xaa	Phe	Asp	Asp	Xaa	Pro	Tyr	Arg	Xaa	Phe	Pro	His	Xaa
	100							105					110		

Arg Ser Ser Met Gly
1 5

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
1 5 10 15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
20 25 30
Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
35 40 45
Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asn Phe
50 55 60
His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
65 70 75 80
Ile Leu Gln Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
85 90 95
Pro Ala Ala Gly Gly Gly Ala
100

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Val Gln Cys Arg Val Trp Leu Gln Ile Gln Trp Arg Gly Met Leu Gly
1 5 10 15


```

Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
    20                      25                      30

Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
    35                      40                      45

Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
    50                      55                      60

Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
    65                      70                      75                      80

Asp Glu Leu Lys Gly Val Thr Ser
    85

```

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Thr Asp Ala Ala Thr Leu Ala Glu Glu Ala Gly Asn Phe Glu Arg Ile
    1                      5                      10                      15

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
    20                      25                      30

Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
    35                      40                      45

Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Glu Lys Gln Glu Leu
    50                      55                      60

Asp Glu Ile Ser Thr Asn Ile Arg Glu Ala Gly Val Glu Tyr Ser Arg
    65                      70                      75                      80

Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
    85                      90                      95

```

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Met Thr Glu Ser Glu Thr Val Thr Val Asp Glu Glu Glu Ile Leu Asn
 1           5           10           15

Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
 20           25           30

Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Glu Glu
 35           40           45

Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
 50           55           60

Lys Glu Arg Glu Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
 65           70           75           80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
 85           90           95

Glu Gly Thr Val Glu Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100           105           110

Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115           120           125

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130           135           140           145

Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Tyr Asn Thr Xaa Thr
145           150           155           160

Leu Thr Leu Glu Gly Asp
165

```

(2) INFORMATION FOR SEQ ID NO:91:

- (1) SEQUENCE CHARACTERISTICS:
- (a) LENGTH: 5 amino acids
 - (b) TYPE: amino acid
 - (c) STRANDEDNESS: single
 - (d) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

Arg Ala Glu Arg Met
1           5

```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 1              5              10              15

Gln Val Arg Val Ala Ala Ala Ala Tyr Gln Thr Ala Tyr Gly Leu Thr
20              25              30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35              40              45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50              55              60

Gln Ala Glu Tyr Gly Gln Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65              70              75              80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85              90              95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Gln Gln Ala
100             105             110

Ala Ala Val Glu Gln Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115             120             125

Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
130             135             140

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145             150             155             160

His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165             170             175

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180             185             190

Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln His Val Gln Thr Ala
195             200             205

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly

```

210	215	220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala		
225	230	235 240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly		
245	250	255
Arg Arg Asn Gly Gly Pro Ala		
260		

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amine acid
- (C) STABILITY: single
- (D) TOPOLOGY: Linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala		
1	5	10 15
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly		
20	25	30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly		
35	40	45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr		
50	55	60
Glu Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro		
65	70	75 80
Val Gly Val Ala Leu Leu Ala Ala Leu Ala Gly Val Val Leu Val		
85	90	95
Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu		
100	105	110
Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr		
115	120	125
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln		
130	135	140
Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr		
145	150	155 160

Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg
 163 170 175
 Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly
 180 185 190
 Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln
 195 200 205
 Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser
 210 215 220
 Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Phe Ala
 225 230 235 240
 Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser
 245 250 255
 Thr Pro Phe Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser
 260 265 270
 Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn
 275 280 285
 Pro Ser Gly Gly Gln Gln Ser Ser Ser Pro Gly Gly Ala Pro Val
 290 295 300

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAAGATGC TGAATCAT CAGCGAAGT CTATCGGGG CAGCTGCAT CAGCCCGCT 60
 GCGCGGCTG TCATCTCAT CAGCGCTGC GGGCGCTCG TATACAGAT GAGCGCGTC 120
 GTCTCGGGG GCGCACTGC GTTGAGGCG GATCGCGCG CTGAGCTTC GACCGCGCC 180
 CAGTTGACCA GGTGTGCA GAGCTCGCC CATCCAGG TGTCTTTTC GAACAAGGC 240
 ATTCTGTTC AGCGCGCAT CCGGGCGCC GAGCGCGCA TCGCGGAC CAACTGAAG 300
 AAGCGCGCG AGCAGCGGA TCTGCGCTG TCTTCAGCG TACGAGAT CCGCGCGCG 360
 GCGCGGGTT CAGCGAGCG CAGCTTTTC GTCTGGGTC CAGAGTCTC GTCCCGGTC 420

AGGACAGACG TCACCTTCTT GATCAAGAGC GGCTGGATGC TCTACACCGC ATGGGCGATG 480
 GAGTTCTCTG AGGCGCGAGC CAACCTGA 507

(2) INFORMATION FOR SEQ ID NO:95:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala 1 15
 5
 Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro 20 25 30
 Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu 35 40 45
 Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser 50 55 60
 Leu Leu Asp Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly 65 70 75 80
 Ser Leu Val Gln Gly Gly Ile Gly Gly Thr Gln Ala Arg Ile Ala Asp 85 90 95
 His Lys Leu Lys Lys Ala Ala Gln His Gly Asp Leu Pro Leu Ser Phe 100 105 110
 Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp 115 120 125
 Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val 130 135 140
 Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met 145 150 155 160
 Gln Leu Leu Gln Ala Ala Gly Asn 165

(2) INFORMATION FOR SEQ ID NO:96:

(1) SEQUENCE CHARACTERISTICS: